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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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85.2	95.4	141.8	147	147	244.2	257.6	259.2	259.2	295.4	327.6	345.6	539.2	574.4	582	585	615	812.4	887	Score
9.6	10.8	16.0	16.6	16.6	27.5	29.0	29.2	29.2	33.3	36.9	39.0	60.8	64.8	65.6	66.0	69.3	91.6	100.0	Query Match Length
160755	243686	240461	202851	168997	1074	1257	1225	1209	456	214669	214669	93287	726	582	585	615	1168	887	Length
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ALIGNMENTS

	CDS	gene		source	FEATURES	JOURNAL	TITLE	AUTHORS	CHWROA	MEDLINE	JOURNAL	AUTHORS	REFERENCE	٧	ORGANISM	SOURCE	VERSION KEYWORDS	ACCESSION	LOCUS	RESULT 1
/gene="BCLB" /note="BCL2 family protein; Boo-like" /codon_start=1 /product="BCLB" /product="BCLB" /protein_id="AAK48715.1" /db_xref="GI:13898394" /translation="WYDOLAERTTWADPLRERTELLLADYLGYCAREPGTPEPAPSTP EAAVLRSAAARLRQIHRSFFSAYLGYPGNRFELVALMADSVLSDSPGPTWGRVVTLVT FAGTILLERGPIVTARWKKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQHRAWLQAQ	50. 664	/map="15q21" 1. 887	/organism="HOMO Sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="15"		Location/Qualifiers	Submitted (07-DEC-2000) The Burnham Institute, 10901 N. Torrey Pines Rd., La Jolla, CA 92037, USA	Direct Submission	Ke,N., Godzik,A. and Reed,J.C.	_	21201065	J. Biol. Chem. 276 (16), 12481-12484 (2001)	<pre>Re,N., Godzik,A. and Reed,J.C.</pre> Rel-R a novel Rel-2 family member that differentially binds and	1 (bases 1 to 887)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Homo sapiens (human)	AF326964.1 GI:13898393	Homo sapiens BCLB (BCLB) mRNA, complete cds. AF326964	AF326964 887 bp mRNA linear PRI 01-MAY-2001	

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SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
OS HOMO Sapiens (human)
PN JP 2002519016-A/12
PD 02-UUL-2002
PP 18-JUN-1999 JP 2000557267
PI SEISHI KATO, TOMOKO KIMURA
PC C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N5/10,C12N15/00,C12N5/
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1168)
Kato,S. and Kimura,T.
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                                           TTCTTCAGGACCCCCTTTCCACTGGCTTTTTGGAGAAAACAGCTGGTCCAGGCTTTTCTG
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Pred. No. 4.8e-131;
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Submitted (05-JUL-2000) University
46, Basel 4057, Switzerland
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BC12-10, a novel anti-apoptotic member of the Bc1-2 family,
blocks apoptosis in the mitochondria death pathway but not in
death receptor pathway
Hum. Mol. Genet. 10 (21), 2329-2339 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 615)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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AF285092
AF285092.1 GI:9837265
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  CTGTTGCTGGCCGACTACCTGGGGTACTGCGCCCGGGAACCCGGGCACCCCGAGCCGGCG
                       CTGTTGCTGGCCACTACCTGGGGTACTGCGCCCCGGGAACCCCGGGCACCCCCGAGCCGGCG
                                                                                   ATGGTTGACCAGTTGCGGGAGCGCACCACCATGGCCGACCCGCTGCGGGAGCGCACCGAG
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                                                        ATGGTTGACCAGTTGCGGGAGCGCACCACCATGGCCGACCCGCTGCGGGAGCGCACCGAG
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                                                                                                                 Conservative
                                                                                                                                                                                   /translation="MVDQLRERTTMADPLRERTELLLADYLGYCAREGTPEEAPSTP
EAAVLESAARLEQIHRSFESAYLGYPGNFELVALMADSVLSSSEGPFMGRVVTLVT
FAGTILLERGPLVTARWEKNGFOPRLKEQEGDVARADCQBLVALLSSRLMGQHRAWLQAQ
GGWDGFCHFFRTPFPLAFWRKQLVQAFLSCLLTTAFIYLWTRLL"
                                                                                                                                                                                                                                            /product="Bcl-2-like protein
/protein_id="AAG00503.1"
/db_xref="GI:9837266"
                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="15"
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l. .615
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100.0%; Pred. No. 8.3e-97;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                          Nrh, a human homologue of Nr-13 associates with inhibitor of apoptosis Oncogene 20 (41), 5846-5855 (2001) 21477277
                                                                                                                                                       Direct Submission
Submitted (23-APR-2002) Gillet
DU VERCORS, 69367, FRANCE
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                     AJ458330
AJ458330.1 GI:20338765
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/gene="NRH"
/function="apoptosis inhibitor"
                                         /gene="NRH"
                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                           Location/Qualifiers
                                                                       chromosome="15"
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Human protein having hydrophobic
BD233456
BD233456.1 GI:33043226
JP 2002519016-A/2.
                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 582)
Kato, S. and Kimura, T.
                Patent:
                                                                                                           Homo sapiens
                                                                                                                          Homo sapiens (human)
              Human protein having hydrophobic domain and Patent: JP 2002519016-A 2 02-JUL-2002;
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CHEMICAL RESEARCH CENTER, PROTEGENE
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/product="anti-apoptotic protein"
/protein_id="CAD30221.1"
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LVTARWKKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQHRAWLQAQGGWDGFCHFF
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PN JP 2002519016-A/2
PD 02-JUL-2002
PF 18-JUN-1999 JP 2000557267
PI SEISHI KATO,TOMOKO KIMURA
PC
C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N5/10,C12N15/00,C12N5/ PC
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CC Human protein having hydrophobic domain and DNA encoding the Same
FT Source Location/Qualifiers
FT Source /organism='Homo sapiens (human)'.
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                                                             38039
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                                 GI:42387450
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REFERENCE AUTHORS

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/mol_type="unassigned DN/
/db_xref="taxon:9606"
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AUTHORS
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On Ju
                                                                                                                                                                                                                                                                                       Note: Data from overlapping BACs AC010674 [drafting center: UWMSC], AC090970 [drafting center: UWMSC], and AC016824 [drafting center: GTC] was added for finishing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 (bases 1 to 93287),
4 (bases 1 to 93287),
Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bl
Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbi
Bate, D. and Hood, L.
Pate, D. and Hood, L.
Direct Submission
Submitted (06-JUL-2001) Multimegabase Sequencing Center,
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (04-JUL-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Ne Pate, D. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-FEB-2000) Multimegabase Sequencing of Washington, PO BOX 357730, Seattle, WA 98195,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 93287)
Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Bird Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of Washington, PO BOX 357730, 3 (bases 1 to 93287)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pate, D. and Hood, L.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Multimegabase Sequencing Center Center code: UWMSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowennsystemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye;
Chemistry: Dye-primer Big Dye; 10%
                                                                                                                                                                                                                                                                                                                                                                   Assembly program:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
consensus was determined from CTD-2184D3 to the extent possible"
1. .8893
                                                          /clone="CTD-2184D3"
/clone_lib="Cal Tech Human BAC library D"
/note="Data from overlapping clones CTD-2650P22 AC090970,
RP11-47K1 AC016824, and RP11-430B1 was added and the
                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="15"
                                                                                                                                      map="15q21.2"
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001 this sequence version replaced
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e 15 clone
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Madan,A., Nesbitt,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gi:12248292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seattle,
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Seattle, WA
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RESULT 8
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                                                     Homo sapiens chromosome 1
SEQUENCE SAMPLING.
AC018903
AC018903.2 GI:8247797
HTG; HTGS_PHASE0.
Homo sapiens (human)
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     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Submitted (22-DEC-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA On Jun 4, 2000 this sequence version replaced gi:6630517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., E
Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,
James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A Madan,A., Nesbitt,R., Shaffer,T. and Hood,L. Sequencing of human chromosome 15 D15S146-D15S117 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Hood, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This record contains 192 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved.
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Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen@systemsbiology.org
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15565;
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6: contig of 1184 bp in length
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8: contig of 802 bp in length
8: gap of unknown length
5: contig of 1147 bp in length
5: gap of unknown length
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8: gap of unknown length
1: contig of 1382 bp in length
1: contig of 818 bp in length
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is contig of 1154 bp in length
is gap of unknown length
contig of 814 bp in length
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is contig of 854 bp in length
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contig of 1243 bp in length
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contig of 1162 bp in length
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n,G.,
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gap of contig

31813: 31913:

gap of contig gap of contig

f unknown length
g of 1126 bp in length
f unknown length
g of 832 bp in length

f unknown length
g of 1266 bp in length
f unknown length
g of 864 bp in length

19875 20701 20801 22087 22037 22137 23124 23124 23127 24197 24297 24297 25142 26386 26486

g of new length
f unknown length
g of 1236 bp in length
of unknown length
or of 887 bp in length

unknown length of 826 bp in length

of unknown length
g of 887 bp in length
of unknown length
g of 1073 bp in length
of unknown length
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f unknown length
f unknown length
g of 1144 bp in length
of unknown length

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28792 29792 29756 30982 31914 31917 33157

gap of contig contig contig contig contig

41845:

f unknown length g of 1206 bp in length f unknown length g of 809 bp in length

gap of contig gap of contig

of unknown length
g of 832 bp in length
by unknown length
ig of 1143 bp in length
ig of 811 bp in length
ig of 851 bp in length
ig of 851 bp in length
ig of 1213 bp in length
if unknown length
if unknown length
if of 128 bp in length
if of 187 bp in length
ig of 188 bp in length
ig of 189 bp in length
ig of 189 bp in length

46114 47031 47031 47031 47131 47131 48292 49276 49276 50389 50489

gap of contig

if unknown length
g of 1110 bp in length
of unknown length
ig of 785 bp in length
of of 1087 bp in length
of of 1087 bp in length
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gap of contig gap of contig gap of contig gap of gap of contig gap of contig

unknown of 1136 unknown

n length 6 bp in length n length

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Bloom, S.,
Madan, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 214669)
2 (bases 1 to 214669)
Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214669 bp DNA linear HTG 04-JUN-2
Homo sapiens chromosome 15 clone RP11-337B11 map 15q21, LOW-PASS
SEQUENCE SAMPLING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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HTG; HTGS_PHASE0.
                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This record contains 192 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 214669)
                                                                                                                                                                                                                                                                                                                                                                                                       the record
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Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: leerowen@systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://chroma.mbt.washington.edu/msg_www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: UWMSC
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4: contig of 1243 bp in length
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                                                                                                                                                                    STS 8140
PCR Profile:
Hot Start:
                                                                                                                                                                                                                                                                      Contact: Spindel ER
Division of Neuroscience
Oregon National Primate Research Center
505 NW 185th Avenue, Beaverton, OR 97006
Tel: 403-690-5388
Fax: 503-690-5384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCL2L10_3137 Rh
clone MMA3137,
                                                                                                                                                                                                                            Email: spindele@ohsu.edu
Primer A: TTTGTCACTTCTTCAGGAC
Primer B: CATGTTTAAAATTAGTCAGCA
                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                     Spindel,E.R., Pauley,M., Jia,Y., Boyle,N., Jiang,S., Gravett,C., Lupo,S.L., Ali,H., Ojeda,S.R. and Norgren,R.B.
Targeted amplification of the 3' end of rhesus macaque orthologs
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
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Macaca mulatta
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                                                                                               Thermal Cycler:
                                                                                                               Extension
                                                                                                                          POR Cycles:
                                                                                                                                                        Annealing:
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4A3137, sequence tagged site.
            Roche)
                                        Primer: dNTP's:
                         Taq Polymerase:
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Total Vol:
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degrees
degrees
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each 200 uM
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for 0.50 min
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KEYWORDS
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                                                           Mus musculus Bcl-2 homolog
AF102501
AF102501.1 GI:4165137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A database containing sequences associated with this project found at: http://rhesusgenechip.unomaha.edu/index.html.
Location/Qualifiers
                                                                                                                      AF102501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rnorgren@unmc.edu
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                                                                                                                                                                                                                                               GGCTCTTCCTTGAGTGAAAGA 886
                                                                                                                                                                                                                                                                                                          TGATGTGGCCAGTGTTTTAACTTGTGACAAGTACTCAGGTGTGAGGACAAGAATGCAAAT
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musculus
                   musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Rhesus macaque genomic DNA"
/dev_stage="Adult"
/note="Organ: Liver; Vector: pGEM-T Eas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="BCL2L10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="genomic DNA"
/strain="Indian orgin"
/db_xref="taxon:9544"
/clone="MMA3137"
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|mol_type="qenomic nna"
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Song, Q.Z., Kuang, Y.P., Dixit, V.M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
1 (bases 1 to 1209)
Song, Q., Kuang, Y., Dixit, V.M. and Vincenz, C.
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                                            CAGCACCGCGCCTGGCTGCAGGCTCAGGGCGGCTGGGATGGCTTTTTGTCACTTCTTCAGG
                                                                                                                             GACGTCGCCCGGGACTGCCAGCGCCTGGTGGTGGTGAGCTCGCGGCTCATGGGG---
                     CGGCACCGCCCAGGCTGGAGGCTCTCGGCGGCTGGGATGGCTTTTTGCCGCTTCTTCAAG
                                                                                                   ATAGTGACCCGAGACTGCTGTCTCATAGTGAACTTTCTGTATAATCTGCTCATGGGGCGT
                                                                                                                                                                                    TACATGGCTGTCAAGCAGAAGA---------GGGATCTGGGGAATCGTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Boo"
/codon_start=1
/codon_start=1
/product="Bcl-2 homolog"
/protein_id="AAD08703.1"
/db_xref="GI:4165138"
/translation="MADSQDPHERTRRILLSDYIFFCAREPDTPERPPTSVEAALLRS
/translation="MADSQDPHERTRRILLSDYIFFCAREPDTPERPPTSVEAALLRS
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PLPLGFWRRLLIQAFLSGFFATAIFFIWKRL"
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/mol_type="mRNA"
/strain="B6D2 F1/J"
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|. .1209
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chromosome="9"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-MAY-1998) | Michigan Medical School,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inohara, N. and Nunez, G. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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(bases 1 to 1225)
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1225
                                                                                                                 /translation="madsqdplherterllsdylffcarepotteppptsveaallrs
vtrqiqqehqeffescesrgnrlelvkqmadkllskoqdfswsqlvmlafagtimn
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                                                                       /gene="Diva"
1225
                                                                                                      1197.
                                                                                                                                                                         /codon_start=1
/product="Bcl-2 homolog"
/protein_id="AAC83150.1"
/db_xref="GI:3955266"
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                     /gene="Diva"
/note="DIVA"
                                                                                                                                                                                                                                                                    /gene="Diva"
143. .718
                                                         /gene="Diva"
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'strain="B6D2F1/J"
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63.1%;
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dical Dr., Ann
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            DB 10;
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                  TGGTGATTTGGCCAGTGTTTTTAACTTGTGACAAGTA 838
                                                         CTGAGGAAGTCCTCCAGCCTAGAGACATTTCTACCTGCATGC-TACATGGAGTTCTGGGT
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TTGTGATGGGGCCAGCATTTGAAAGGGGCCCCATGTA
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1257)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

ACCESSION VERSION KEYWORDS

BC052690.1 MGC.

GI:30851238

BC052690

RESULT 13 BC052690 LOCUS

DEFINITION

BC052690 1257 bp Mus musculus Bcl2-like 10, mRNA IMAGE:30052580), complete cds.

mRNA (cDNA clone

linear ROD e MGC:60542

08-OCT-2003

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REMARK
COMMENT
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TITLE
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Yulan Piao and Minoru Ko (National Institute on Aging, NIH: http://lgsun.grc.nia.nih.gov/cDNA/) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/
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cDNA Li
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7304926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Bietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Procurement: Minoru Ko
                                                                                                                                                                                                                                                                                  /db xref="taxon:10090"
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(Long)"
                                                                                             / db_xref="MGI:1330841"
145. .720
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                                                                                                                                                                                                                                note="Vector: pSPORT1"
                                                                                                                                                                                                                                                                                                                                                                                              strain="C57BL/6J"
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                                                                                                                                                                                                                                     CTGAGGAAGTCCTCCAGCCTAGAGACATTTCTACCTGCATGC
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TTGTGATGGGGCCAGCATTTGAAAGGGGCCCCATGTA
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'db_xref="CDD:smart00337"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Itoh,T., Itoh,A. and Pleasure,D.
BC1-2-related protein family gene expression
oligodendroglial differentiation
J. Neurochem. 85 (6), 1500-1512 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Itoh, T., Itoh, A. and Pleasure,
Direct Submission
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GAGGCGACGTCGCCGGGACTGCCAGCGCCTTGGTGGCCTTGCTGAGCTCGCGGCTCATG
                                                                                                                                                                                                                                                    TCCGCGGCCAGGTTACGGCAGATTCACCGGGTCCTTTTTCTCCGGCCTACCTCGGCTAC
                                                                                                                                                                                                                                                                                                               GCCCGGGAACCCGGGAGCCGGCGGCGCCATCCACGCCCGAGGCCGCCGTGCTGCGC 199
                                                                                                                                                                                                                                                                                                                                                          GACAGGACTGTTAAGCGGAGGAGGGATCAAAGAAACCGTCTCCTAC
                                                                                                                                        GGCCCCACCTGGGGCAGAGTGGTGACGCTCGTGACCTTCGCAGGGACGCTGCTGGAGAGA 379
                                                                                                                                                                      CAGGGCAACCGCCTGGAGCTGGTGACACAGATGGCGGATGAGTTGCTCTCCAATGACCAA
                                                                                                                                                                                                   CCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGTGCTCTCCGACAGCCCC 319
                                                                                                                                                                                                                                   TCTGTGACTAGTCAGATCCAACAGGAGCACCAGGATCTTTTCAACTCCTTCCGCGACTAC
                                                                                                                                                                                                                                                                                                                                                                                      ATGGCCGACCCGCTGCGGGAGCGCACCGAGCTGTTGCTGGCCGACTACCTGGGTACTGC
                                                                             GGGCCGCTGGTGACCGCCCGGTGGAAGAAGTGGGGCTTCCAGCCGCGGCTAAAGGAGCAG
                                                                                                            GAGTTCAACTGGGGCCGCCTGGTGATGCTCCTGGCCTTCGTGGGGACGCTAATGAACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="BCL2L10"
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/protein id="AAK31792.1"
/protein id="AAK31792.1"
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/translation="MGDPLQDRTRRLLIDYILFCARAFNTPEPLPTSVEAALLRSVTS
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TVKRRRDQRNRLLLERDCYLIVSLLYNRLTGRHRSWLEAHGGWDGFCQFFKNPLPPGF
WRRLLIRAILSCFFATAIFYIWKCL"
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12. .569
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/codon_start=1
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strain="Sprague-Dawley"
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0; Mismatches 253
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AC133947
AC133947.3 GI:51921460
                                                                                                        Center project name: M_BB0189I02
                                                                                                                                                                      Center: Washington University Center code: WUGSC
                                                                                                                                                                                                                                Submitted (08-SEP-2004) Genome Sequencing Parkway, St. Louis, MO 63108, USA On Sep 8, 2004 this sequence version repla
                                                                                                                                                                                                                                                                                                            Parkway, St. Louis, MO
4 (bases 1 to 168997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 168997) McPherson, J.D. and Wat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence of Mus musculus Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 168997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                        Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                            Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUL-2004)
                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                     Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-SEP-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                      Web site:http://genome.wustl.edu
                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                      Parkway, St.
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                                                                                                                                                                                                                                                                                                                                                                                     kway, St. Louis, MO (bases 1 to 168997)
   /mol_type="genomic DNA
/db_xref="taxon:10090"
/chromosome="9"
                               organism="Mus musculus"
|mol_type="genomic DNA"
                                                                          Location/Qualifiers
                                                               .16899
                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Waterston, R.H.
                                                                                                                                                                                                      Genome Center
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Sciurognathi;
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GAACTGAGGAAATCCTCCTGCCTAGAGACATTTCTACCTGCATGC-TACACGGAGTTCCG
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New isolated or recombinant Bcl-B nucleic acids and polypeptides, for

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Best Local Similarity
Matches 582; Conserv
31-JAN-2001; 2001WO-US003080.
                                                09-AUG-2001.
                                                                                              WO200157060-A1
                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                           immunosuppressive; antiinflammatory; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                    Bcl-2-like polypeptide; autoimmune disorder; allergy; immunomodulatory;
respiratory; cardiovascular; antiarthritic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                       Human Bcl-2-like polypeptide encoding cDNA (clone HLIBE40)
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                                                                                                                                         /*tag= a
/product= "Bcl-2-like polypeptide"
/note= "gene No. 2"
                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C? The invention provides nucleic acid molecules (NAMI) encoding 4 human Bcl c? -like polypeptides (PEP1). The NAMI and PEP1 may be used in the CC prevention, diagnosis and treatment of diseases associated with the CC inappropriate Bcl-2-like polypeptides' expression. The NAMI may be used CC inappropriate Bcl-2-like polypeptides expression and artice in the CC methodolgy. The polypeptides may also be used as antigens in the CC production of antibodies against Bcl-2 and in assays to identify CC modulators of Bcl-2 expression and activity. The anti-Bcl-2 antibodies and antagonists may be used to down regulate expression and activity. The anti-Bcl-2 antibodies CC and anti-Bcl antibodies may also be used as diagnostic agents for detecting CC immunosorbant assay (ELISA). Disorders that may be prevented, diagnosed CC immunosorbant assay (ELISA). Disorders that may be prevented, diagnosed CC and/or treated by the above methods include, immunodeficiencies (e.g. a cc gammaglobulinemia and B cell lymphoproliferative disorder), autoimmune CC disorders (e.g. rheumatoid arthritis and Grave's disease), altergic CC reactions, inflammations, respiratory diseases and cardiovascular CC disorders (a full list of disorders is given in the specification). The CC present sequence represents a human Bcl-2-like polypeptide encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 276; 285pp; English
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07-FEB-2000;
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                                                  ACCTGCCCAACTGTGACCAACTAAATGACAGATGTGTGAGAACAAGAACTGAGGGAAAGC
                                                                                                                      CAGCCTTCATTTATCTCTGGACACGATTATTATGAGTTTTAAAAACTTTTAACCCGCTTCT
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llarity 99.4%;
Conservative
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2000US-0180697P
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Pred. No. 3.2e-104;
0; Mismatches 2;
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420

480

ABK41913 standard; CDNA; 548 BP. ABK41913; 21-WAY-2002 (first entry) CDNA encoding novel human connective tissue related human; connective tissue related disorder; cancer; g cytostatic; gene; ss. Homo sapiens. WC200155343-A1. 02-AUG-2001. 17-JAN-2001; 2000US-0179055P. 04-FEB-2000; 2000US-018655P. 04-FEB-2000; 2000US-018655P. 04-FEB-2000; 2000US-018655P. 04-FEB-2000; 2000US-018655P. 04-FEB-2000; 2000US-018655P. 04-FEB-2000; 2000US-01865P. 0	Qy 750 ACCTTCCCCCACACCC-TTTTTATCTGAATGCATACAA 790
PR 18-SEP-2000; PR 14-SEP-2000; PR 21-SEP-2000; PR 21-SEP-2000; PR 22-SEP-2000; PR 23-SEP-2000; PR 23-SEP-2000	SEP-2000; SEP-2000; SEP-2000;
0.233298 0.233298 0.233298 0.233290 0.233240 0.233240 0.233260 0.233260 0.234223 0.234223 0.234223 0.234223 0.235669 0.235699 0.2356	2000US-0231413P. 2000US-0231414P. 2000US-0232080P.

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17-NOV-2000;
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the isolation of novel human connective tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide (cDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK41613-ABK42101 represent cDNA sequences encoding the novel human connective tissue related polypeptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; SEQ ID NO 311; 673pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cleic acid encoding novel connective tissue associated polypeptides, ed in diagnosing, preventing, treating or ameliorating a disorder su cancer or rheumatoid arthritis.
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                                                                                                                                                                                                                                                               CGGCCCACCTGGGGCAGAGTGGTGACGCTCGTGACAACGCTGCTGGAGAG
                                                                                                                                                                                                                                                                                                                  CTTGTTAACAACAGCCTTCATTTATCTCTGGACACGATTATTATGAGTTTTAAAAACTTTT
                                            CAGGACCCCCTTTCCACTGGCTTTTTGGAGAAAACAGCTGGTCCAGGCTTTTTCTGTCATG
                                                                               GGGCAGCACCG-GCCTGGCTGCARGCTCAGGGCGGCTGGGATGGCTTTTGTCACTTCTT
                                                                                                          GGGGCAGCACCGCCCTGGCTGCAGGCTCAGGGCGGCTGGGATGGCTTTTGTCACTTCTT
                                                                                                                                     GGAGGGCGACGTCGCCSGGGACTGCCAGCGCCTGGTGGCCTTGCTGAGCTCGCGGCTCAT
                                                                                                                                                               GGAGGGCGACGTCGCCGGGACTGCCAGCGCCTGGTGGCCTTGCTGAGCTCGCGGCTCAT
                                                                                                                                                                                                         AGGGCCGCTGGTGACCGCCCGGTGGAAGAAGTGGGGCTTCCAGCCGCGGCTAAAGGAGCA
                                                                                                                                                                                                                                               CGGCCCCACCT-GGGCAGAGTGGTGACGCTCGTGACCTTCGCAGGGACGCTGCTGGAGAG
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2000US-0251030P.
2000US-0251988P.
2000US-0256719P.
2000US-0251859P.
2000US-0251868P.
2000US-0251989P.
2000US-0251999P.
2000US-0251999P.
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2000US-0249300P.
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Pred. No. 4.6e
2; Mismatches
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.4.6e-93;
5;
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KW antiinflammatory; antiallergic; antiasthmatic; deermatological;
KW nephrotopic; virucide; fungicide; antibacterial; antiparasitic;
KW gene therapy; ds; connective tissues disorder; rheumatoid arthritis;
KW cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder;
KW cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder;
KW Altheimer's disease; Parkinson's disease; cardiovascular disease;
KW Altheimer's disease; Parkinson's disease; cardiovascular disease;
KW whintis; eczema; inflammatory condition; Crohn's disease; nephritis;
KW astrointestinal disorder; inflammatory bowel disease; nephritis;
KW agstrointestinal disorder; inflammatory bowel disease;
KW v-linked lymphoproliferative syndrome;
KW v-linked lymphoproliferative syndrome;
KW chromosome identification; chromosome mapping;
KW connective tissue related polynucleotide; gene; ss.
                                                                         14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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07-JUL-2000;
07-JUL-2000;
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19-MAY-2000;
07-JUN-2000;
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2000US-018464P.
2000US-0189874P.
2000US-0199076P.
2000US-0199076P.
2000US-020515P.
2000US-021513P.
2000US-0215135P.
2000US-021647P.
2000US-0217487P.
2000US-0225148P.
2000US-0225214P.
2000US-0225214P.
2000US-0225266P.
2000US-0225266P.
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The invention describes an isolated nucleic acid molecule (I), which comprises a sequence that is at least 95 % identical to a connective tissue-related polynucleotide encoding connective tissue antigens (CTA). The polypeptide or polynucleotide is useful for preventing, treating, or ameliorating medical conditions in a mammal. The connective tissue polypeptides, polynucleotides and antibodies are particularly useful for treating, preventing and/or prognosing disorders of connective tissues (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus, scleroderma, or Sjogren's Syndrome), cancers, cancer metastases and/or neoplasias (e.g. leukaemia), neurodegenerative disorders (e.g. Alzheimer's disease, or Parkinson's disease), cardiovascular diseases (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass complications), autoimmune diseases (e.g. systemic lupus erythematosus, rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.
   Query Match
Best Local Similarity 98.3
Matches 481; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
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08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                          New connective tissue-related polypeptides and polynucleotides, useful for treating, preventing and/or prognosing e.g. disorders of connective tissue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or neoplasias.
                                                                                                                                                                                                                                                                                                Claim
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DB; ADB60069.
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2000US-0246639P.
2000US-0246610P.
2000US-0246611P.
2000US-0249208P.
2000US-0249210P.
2000US-0249211P.
2000US-0249218P.
2000US-0249219P.
2000US-0249219P.
2000US-0249249P.
2000US-025929P.
2000US-025929P.
2000US-0251868P.
2000US-0251868P.
2000US-0251868P.
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2000US-0251989P.
2000US-0251990P.
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                                                                                                                                                                                                                                                                                              NO 311; 248pp; English.
                51.5%;
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Score 457.2; DB 9;
Pred. No. 4.6e-93;
2; Mismatches 5;
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   Indels
                            Length 548;
   2
   Gaps
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14-AUG-2000
14-AUG-2000
14-AUG-2000
14-AUG-2000
14-AUG-2000
18-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
01-SEP-2000
01-SEP

2000US. 2000US

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2000US-0225470P
2000US-0225475P
2000US-022575P
2000US-022575P
2000US-022575P
2000US-0226881P
2000US-0226881P
2000US-0227108P
2000US-0227108P
2000US-0227182P
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2000US-023943P
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          Determining the degree of cytosine methylation in genomic DNA, diagnosis and prognosis, comprises selective hybridization of from chemically treated DNA.
                                                                                                                        01-SEP-2000; 2000DE-01043826.
05-SEP-2000; 2000DE-01044543.
                                                                                                                                                            01-SEP-2001;
                                                                                                                                                                                                         WO200218632-A2
                                                                                                                                                                                                                                                   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                          Oligonucleotide for detecting cytosine methylation SEQ ID NO 30995.
                                                                                                                                                                                                                                                                                                                                  12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                              ABQ44404 standard; DNA;
                                                       2002-371829/40
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                                                                                                    EPIGENOMICS
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Claim 12; 56pp + Sequence Listing; 56pp;
  German.
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This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CDNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the CC degree of hybridisation to both classes is determined from the label on CC oligomers, the degree of methylation is calculated. The method is used: CC oligomers, the degree of methylation is calculated. The method is used: CC oligomers, cardiovascular, gastrointestinal and respiratory systems etc., CC particularly by detecting mutations or side effects of therapeutic drugs CC nervous, cardiovascular, gastrointestinal and respiratory systems etc., CC particularly by detecting mutations or single nucleotide polymorphisms CC (SNP's); and (ii) for differentiation of cell or tissue types and for crowstigating cell differentiation. The method allows the methylation CC status of many C residues to be determined simultaneously. ABQ13410-CC ABQ54121 represent genomic DNA sequences used to illustrate the method CC disclosure of the invention member,

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Sequence
 874
BP; 144 A; 90 C; 320 G; 320 T; 0 U; 0 Other;
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밁 밁 밁 Query Match Best Local S Matches 405 481 520 421 460 361 400 301 340 241 280 181 220 121 100 160 61 h 36.6%; Similarity 75.1%; CGAGGCCGCCGTGCTGCGCTCCGCGGCCGCCGCCAGGTTACGGCAGATTCACCGGTCCTTTTT GTTGCGGGAGCGACCACCATGGCCGACCCGCTGCCGGGGAGCGCACCGAGCTGTTGCTGGC GCTGAGCTCGCGGCTCATGGGGCAGCACCGCGCCTGGCTGCAGGCTCAGGGCGGCTGGG 539 GCCGCGGCTAAAGGAGCAGGAGGGGCGACGTCGCCCGGGACTGCCCAGCGCCTTT AGGGACGCTGCTGGAGAGAGGGCCGCTGGTGACCGCCCGGTGGAAGAAGTGGGGCTTCCA cerecrereceacaecececeacereceaecaeaereereacecreereacerrece CTCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTC CGATTATTTGGGGTATTGCGTTCGGGAATTCGGTATTTTCGAGTCGGCGTTATTTACGTT CGACTACCTGGGGTACTGCGCCCGGGAACCCCGGCAGCCGGGCGCCATCCACGCC GTTGCGGGAGCGTATTATTATGGTCGATTCGTTGCGGGAGCGTATCGAGTTGTTGGT CGGGTTAAGAAAATTAGCGAAGGTTCGGTTTTTTAGTAGAGGTCGGATTATGGTTGATTA 159 GTCGCGGTTAAAGGAGTAGGAGGGCGACGTCGTTCGGGATTGTTAGCGTTTGGTGGTTTT AGGGACGTTGTTGGAGAGAGGGTCGTTGGTGATCGTTCGGTGGAAGAAGTGGGGTTTTTTA CGTGTTTTTCGATAGTTTCGGTTTTATTTGGGGTAGAGTGGTGACGTTCGTGATTTTCGT TTTCGTTTATTTCGGTTATTTCGGGAATCGTTTCGAGTTGGTGGCGTTGATGGCGGATTT Conservative <u>,</u> Score 324.6; DB 6; Length 8 Pred. No. 3.3e-63; 0; Mismatches 134; Indels 874; 0, Gaps 339 219 519 459 360 300 180 579 399 240

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GTTGAGTTCGCGGTTTATGGGGTAGTATCGCGTTTGGTTGTAGGTTTAGGGCGGTTGGG

638

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ABQ44405 standard; DNA; 874

RESULT 8
ABQ44405/c
ID ABQ444
XX
AC ABQ444
XX
AC ABQ444
XX
DT 12-JUL ABQ44405;

12-JUL-2002 (first entry)

Oligonucleotide for detecting cytosine methylation

SEQ ID

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30996.

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This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, co of oligonuclectides and/or peptide-nucleic acid (PNA) oligoners and the correct of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of coligoners, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs are of a wide range of diseases, e.g. cancer, disorders of the central concervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SPF's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABBJ3410-ABBJ411 represent genomic DNA sequences used to illustrate the method for the corribed in the method corribed in the method in the met
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05-SEP-2000;
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CGAGGCCGCCGTGCTGCGCCCCGCCGCCCAGGTTACGGCAGATTCACCGGTCCTTTTT
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                                                                                                  CGATTATTTGGGGTATTGCGTTCGGGAATTCGGTATTTTCGAGTCGGCGTTATTTACGTT
                                                                                                                                                                            CGACTACCTGGGGTACTGCGCCCGGGAACCCGGCACCCCGAGCCGGCGCCATCCACGCC
                                                                                                                                                                                                                                                   GTTGCGGGAGCGTATTATTATGGTCGATTCGTTGCGGGAGCGTATCGAGTTGTTGGT
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2000DE-01044543.
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Pred. No. 3.3
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc.,

Determining the degree of cytosine diagnosis and prognosis, comprises

methylation in genomic DNA, useful for selective hybridization of amplicons

chemically treated

DNA.

Claim 12; 56pp + Sequence Listing; 56pp; German.

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ARESULT 9
ABQ44403
ID ABQ44403
AC ABQ4
AC Olig
AC ABQ4
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05-SEP-2000;
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                                                                                              Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention
 01-SEP-2001; 2001WO-EP010074.
                          07-MAR-2002
                                                WO200218632-A2
                                                                                                                                                          Oligonucleotide
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Pred. No. 3.6e-62;
                                                                                                                                                          cytosine methylation SEQ ID
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Best Local S
Matches 401
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Sequence

874

BP; 119 A; 90 C; 291 G;

374 T; 0 U; 0 Other;

h 36.1%; Similarity 74.8%;

Conservative

<u>.</u>

Score 320; DB 6; I Pred. No. 3.6e-62; 0; Mismatches 135;

Length 874; Indels

0

Gaps

475 301 535 241

421

GCCGCGGCTAAAGGAGCAGGAGGGCGACGTCGCCCGGGACTGCCAGCGCCTTGGTGGCCTTT

480

356 420 416 360 476

AGGGACGCTGCTGGAGAGAGGGCCGCTGGTGACCGCCCGGTGGAAGAAGTGGGGCTTCCA 181

CGAGGCCGCGTGCTGCGCTCCGCGGGCCGGCCAGGTTACGGCAGATTCACCGGTCCTTTTT

CGAAACCGCCGTACTACGCTCCGCGACCGCCAAATTACGACAAATTCACCGATCCTTTTT

CTCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTC

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180 656

CGTGCTCTCCGACAGCCCCGGCCCCACCTGGGGCAGAGTGGTGACGCTCGTGACCTTCGC CTCCGCCTACCTCGACTACCCCGAAAACCGCTTCGAACTAATAACGCTAATAACGAATTC 121 715

CGACTACCTGGGGTACTGCGCCCGGGGAACCCCGGGCACCCGAGCCGGCCCATCCACGCC

CGACTACCTAAAATACTACGCCCGAAAACCCGGACACCCCGAACCGACGCCATCCACGCC

775

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61 GTTGCGGGAGCGCACCACCATGGCCGACCCGCTGCGGGAGCGCACCCGAGCTGTTGCTGGC

ATTACGABAACGCACCATAACCGACCCGCTACGABAACGCACCGBACTATTACTBAC

CGAACCAAAAAAACCAACGAAAACCCGACCCCCAACAAAAACCGAACCATAATTAACCA 716

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This invention describes a novel method for determining the degree of comethylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of cityomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs cand of a wide range of diseases, e.g. cancer, disorders of the central corrous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation contents to be determined simultaneously. AB013410-
ABQ54121 represent genomic DNA sequences used to illustrate for determining the degree of cytosine methylation described disclosure of the invention
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05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; 56pp + Sequence Listing; 56pp; German.
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2000DE-01044543.
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                                                                                                                                                                                                             The invention relates to a novel array comprising at least two isolated CC nucleotide molecules, each molecule having a sequence capable of uniquely CC hybridising to a nucleic acid molecule which is an expression product of cc a gene involved in mitochondrial biology. The array comprises two or more isolated nucleic acid molecules or spots, each molecule having a sequence CC chosen from sequence of 994 human probes and 2046 mouse probes. An array CC with the sample under conditions allowing selective hybridisation, and CC measuring hybridisation of nucleic acid in the sample to the array to CC produce an expression profile. The array is also useful for determining CC an expression profile of a first labelled sample containing nucleic acid crelative to a second sample is a reference or a standard. An array is useful for determining an expression profile diagnostic of an energy-metabolism CC relative to a second sample is a reference or a standard. An array is useful for determining an expression profile diagnostic of an energy-metabolism CC contest the physiological condition. An array of the invention is useful for determining mitochondrial biology gene expression profiles of organisms, which are useful for determining micoandition. An array of the invention is useful couch as human, mice and closely related species, tissue and organs of couch as summan, mice and closely related species, tissue and organs of couch account which are useful for determining expression profiles containing expressi
                                                                      diagnosing such physiological conditions, identifying biochemical pathways, genes, and mutations involved in such physiological conditions, identifying therapeutic agents useful for preventing and/or treating such physiological conditions, evaluating and/or monitoring the efficacy of such therapies, and creating and identifying animal models of human energy metabolism-related physiological conditions. An array is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Array containing probes for genes involved in mitochondrial biology, useful for determining mitochondrial biology gene expression profiles use in diagnosing pathologies and identifying biochemical pathways.
useful for defining expression signatures or profiles for mitochondrial diseases, as well as distinguishing clinical disorders that result from oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-300821/29
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31-AUG-2001;
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mitochondrial disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse mitochondrial DNA sequence SEQ ID NO:1910
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                                                                                      TTAACAACAGCCTTCATTTATCTCTGGACACGATTATTATGAGTTTTTAAAACTTTTTAACC
                                                                                                                                   AATCCTTTACCGCTCGGCTTCTGGAGAAGATTGCTGATTCAGGCTTTTCTGTCAGGCTTC
                                                                                                                                                              ACCCCCTTTCCACTGGCTTTTTGGAGAAAACAGCTGGTCCAGGCTTTTCTGTCATGCTTG
                                                                                                                                                                                                                                                                      ATAGTGACCCGAGACTGCTGTCTCATAGTGAACTTTCTGTATAATCTGCTCATGGGGCGT
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 CGATCTTACCTACCTGCGGAACCCCTCTAAGGACAATTCTGGG
                               CGCTTCTACCTGCCCAACTGTGACCAACTAAATGACAGATGTGTG
                                                                 TTTGCAACAGCCATCTTTTTTATCTGGAAACGTTTAT-
                                                                                                                                                                                                    CGGCACCGCCAGGCTGGAGGCTCTCGGCGGCTGGGATGGCTTTTTGCCGCTTCTTCAAG
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Pred. No. 3e-44;
D; Mismatches 2
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RESULT 12
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Mouse mitochondrial DNA sequence SEQ ID NO:2360.

15-JAN-2004

(first

entry)

oxidative stress; apoptosis; aging. mitochondrial array; mitochondrial; hybridisation; disease; oxidative phosphorylation energy-metabolism; dysfunction;

Mus musculus

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for defining expression signatures or profiles for mitochondrial diseases, as well as distinguishing clinical disorders that result from oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress, apoptosis and aging. An array of the invention contains probes of genes not previously recognised to participate in mitochondrial biology. The sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA clones used to make the probes of the invention. Some sequences are not present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostic of energy metabolism-related physiological conditions, diagnosing such physiological conditions, identifying biochemical pathways, genes, and mutations involved in such physiological conditions, identifying therapeutic agents useful for preventing and/or treating such physiological conditions, evaluating and/or monitoring the efficacy of such therapies, and creating and identifying animal models of human energy metabolism-related physiological conditions. An array is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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TGGGG----CAGCACCGCGCCTGGCTGCAGGCTCAGGGCGGCTGGGATGGCTTTTGTCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 154; DB 10;
Pred. No. 7.7e-25;
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The invention relates to a novel array comprising at least two isolated nucleotide molecules, each molecule having a sequence capable of uniquely hybridising to a nucleic acid molecule which is an expression product of a gene involved in mitochondrial biology. The array comprises two or more isolated nucleic acid molecules or spots, each molecule having a sequence chosen from sequence of 994 human probes and 2046 mouse probes. An array of the invention is useful for determining an expression profile of a mouse or human sample containing nucleic acid, by contacting the array with the sample under conditions allowing selective hybridisation, and measuring hybridisation of nucleic acid in the sample to the array to produce an expression profile. The array is also useful for determining an expression profile of a first labelled sample containing nucleic acid
                                                                                                                                                                                                                                                     Array containing probes for genes involved in mitochondrial biology, useful for determining mitochondrial biology gene expression profiles use in diagnosing pathologies and identifying biochemical pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-2001;
31-AUG-2001;
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mitochondrial disease; oxidative phosphorylation
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2001CA-02356540.
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                                                                                                                                                                                                                       2361; 201pp;
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n dysfunction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for defining expression signatures or profiles for mitochondrial diseases, as well as distinguishing clinical disorders that result from oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress, apoptosis and aging. An array of the invention contains probes of genes not previously recognised to participate in mitochondrial biology. The sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA clones used to make the probes of the invention. Some sequences are not present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905, 1906, 2408 and 2643.
                                                                                                                                                                                                                         gene;
                                                                                                                                                                                                                                                                        Rice gene,
 Chang H,
                                                                                                                              03-JAN-2003
                                                                                                                                                             WO2003000898-A1
                                                                                                                                                                                           Oryza sativa
                                                                                                                                                                                                                                        Plant; bacterial
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                                 (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                               22-JUN-2001; 2001WO-IB001105
                                                                                              22-JUN-2001; 2001WO-IB001105
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 Chen W,
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 ATGAGTTTTAAAACTTTTAAACCCGCTTCTACCTGCCCAACTGTGACCAACTAAAATGACAG
                                                                                                                              TTTTGTCACTTCTTCAGGACCCCCTTTCCACTGGCTTTTTGGAGAAAACAGCTGGTCCAG
                                 CRKCASKRSSAKRYAMMGGMTSGSRMSRWKSYTCYWRKWGSMKSTCTWMYYMSKYTYAKY
                                                                                              KRMYMYKMWWYKRKYSKCSWYCKMSYYASCMKSARKAGAKMCKRSKMSAWSKSMRSSRK
                                                                                                                                                             CRRRWGRMYRMRWKRYYMSARYTMRYCARKKYSYSAARKARCWYRGKGYYWAGMWMKRY
                                                                                                                                                                                          CTCGCGGCTCATGGGGCAGCACCGCGCCTGGCTGC--AGGCTCAGGGCGGCTGGGATGGC
                                                                                                                                                                                                                         GMMRWKSWKRMASKYKWMSRMYRWRKKKKCSRTTMWGKTRGGMMGTMGRCRYKKRSGMKRK
                                                                                                                                                                                                                                                       GCTAAAGGAGCAGGAGGGCGACGTCGCCCGGGACTGCCCAGCGCCTGGTGGCCTTGCTGAG
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Identifying at least
              WPI; 2003-175290/17.
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                             Tao
                             Whitham
                            ß
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                             o.
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pathogenic infection bacterial, fungal or one gene involved in plant resistance or r for conferring resistance or tolerance to viral infection by determining or detectir istance or response olerance to a plant or detecting plant 6 6

27; SEQ ID NO 5263; 899pp; English

comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression for identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

8

Length 2000,

86; Similarity AAGAAAACCAGCGAAGGCCCGGCCCCCAGCAGAGGCCGGACCATGGTTGACCAGTTGCG Conservative 7.7%; 362; Score 68; DB Pred. No. 2e-0 62; Mismatches 2e-05; 322; Indels 12; Gaps ω

146 MWCYARGCGSCKRKKSKGGSWGKTCRRGA-----RGGSGWSSGAKYKSGSMSKRMWMSS 26 MMSCARMGSSRMSRKMGSMSKYRKĆSSĆGKĆKMTTRRKSKWYSASSASGRTGSKWSSGSY SGKGMKKRYKRSKRWRGRGRRGMRRSRMRWMGRYRRCARSGRMAGGSGRMMGGKSRMSYW SRTSRRKKRKWCMRKRKYKRMRGYSRMRSCKRARWMKRCRSGRAWKWGCRGCMTCRMKSY GCTGCTGGAGAGAGGGCCGCTGGTGACCGCCCGGTGGAAGAAGTGGGGCTTCCAGCCGCG SRMAMMYKKMYWYRGYKGMKRGWWAGRMMRSMCRWSKACYYMRWRWRMTRRRRWAKKS CTCCGACAGCCCCGGCCCCACCTGGGGCAGAGTGGTGACGCTCGTGACCTTCGCAGGGAC CTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGTGCT 306 CCTGGGGTACTGCGCCCGGGAACCCGGGCACCCCGAGCCGCGCCATCCACGCCCGAGGC 186 GGAGCGCACCATGGCCGACCCGCTGCGGGAGCGCACCGAGCTGTTGCTGGCCGACTA 126 SMMWKMMRKMRWSRSYGWYSWSYKMWMCTAYKKSYYSRWCYMYRGGGWRGATRYWGRGYM CGCCGTGCTGCGCTCCGCCGCCCAGGTTACGGCAGATTCACCGGTCCTTTTTCTCCGC CGRSGCGRRSAYSRYYGTSRKYGTYKKMTYYSASRCMRAYMTTSYSWACSSYTWCRSKRR 366 439 319 426 246 145 85 379 199

-GCTTTTCTGTCATGCTTGATTAACAACAGCCTTCATTTATCTCTGGACACGATTATT 660

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RESULT 15
ABN42801
The present invention describes oligonucleotide libraries for detecting CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple CC transcripton units that populate a genome. The library comprises several CC oligonucleotides, each capable of hybridising selectively to a set of CC messenger RNAs transcribed from a given transcription unit of the genome, CC which encodes one or more messenger RNA splice variants. The CC oligonucleotide libraries are useful for detecting mRNAs from a CC biological sample, in expression profiling studies, in qualitatively or CC quantitatively characterising the corresponding transcriptome, and in CC transcriptomes. The libraries may also be used as specialised mini CC transcriptomes. The libraries may also be used as specialised mini CC libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue cand pathology-specific genes such as those genes only expressed in CC specific tissue under a specific pathological condition, to detect cand pathology-specific pathological condition, to detect variants of a transcriptome of a patient suffering from a particular consecution. No. The sequence used in the exemplification of the printed specification, but was obtained in electronic format CC directly from WIPO at fig.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID NO 15549; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-257383/30
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02-MAY-2001; 2001US-0287724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-2001; 2001WO-IB001903.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COMP-) COMPUGEN INC
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RY 801
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밁 გ S Matches Query Match Best Local Sequence 60 BP; 9 565 CCCCTTTCCACTGGCTTTTTGGAGAAAACAGCTGGTCCAGGCTTTTTCTGTCATGCTTGTT 60; _ Similarity CCCCTTTCCACTGGCTTTTTGGAGAAAACAGCTGGTCCAGGCTTTTCTGTCATGCTTGTT 6.8%; larity 100.0%; Conservative (A; 16 C; 13 G; 22 T; 0 U; 0 Other; 0; Score 60; Pred. No. Mismatches DB 6; 1 0 Length 60; 0; Gaps 60

Search completed: June 7, Job time: 871.812 secs 2005, 22:14:33

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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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9
             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1: uniprot_sprot:*
2: uniprot_trembl:*
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       BAXA RAT
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ROM N.A. (477277; PubMed=11593390; Do (477277; PubMed=11593390; Do (477277; PubMed=11593390; Do (477277; PubMed=11593390; Do (5846-5855(2001); (60): Promotes cell survival (60): Promotes cell survival (70): Bands to Bcl-2, Bcl-X an (71): Binds to Bcl-2, Bcl-X an (72): Binds to Bcl-2 wepres (73): PROTECTIY: Widely expres (8): PROTECTIY: Widely expres (8): PROTECTIY: Contains 1 Bcl-2 home (8): PROTECTIY: Contains 1 Bcl-2 home (8): PROTECTIY: Institute of Biolian (8): PROTECTIY: Institutions as	SQUENCE FROM N.A. ISSUE=COVARY; SDLINE=21548034; PubMed=11689480; D SDLINE=21548034; PubMed=11689480; D SDLINE=21548034; PubMed=11689480; D SQUENCE FROM N.A. ISSUE=Liver; SULINE=21201065; PubMed=11278245; D N., Godzik A., Reed J.C.; SCIB-B, a novel Bcl-2 family member SQUIATES Bax and Bak."; Biol. Chem. 276:12481-12484 (2001)	RESULT 1 BCLB HUMAN STANDARD; PRT; 194 ID BCLB HUMAN STANDARD; PRT; 194 AC Q9HD36; Q8TCS9; DT 28-FEB-2003 (Rel. 41, Created) DT 28-FEB-2003 (Rel. 41, Last sequence upda DT 05-JUL-2004 (Rel. 44, Last annotation up E Apoptosis regulator Bcl-B (Bcl-2-like 10 DE Protein NrH). GN Name=BCL2L10; Synonyms=BCLB; OS Homo sapiens (Human). OC Mammalia; Eutheria; Primates; Catarrhini OX NCBI TaxID=9606; RN (11 -	32 113 10.4 114 2 Q9NR76 33 113 10.4 143 1 BAXD HUMAN 34 113 10.4 178 2 Q8CFR2 35 113 10.4 178 2 Q9CYM5 36 112.5 10.4 228 1 AR1_XENLA 37 111.5 10.3 175 2 Q925A9 38 111 10.2 193 2 Q88996 40 111 10.2 219 2 Q7TS60 40 111 10.2 350 2 Q8TYS5 41 109 10.1 239 1 BCL2_HUMAN 42 107 5 9.9 193 2 Q8CGL4 43 107.5 9.9 193 2 Q8CGL4 44 107 9.9 350 1 MCL1_HUMAN 45 107 9.9 350 1 MCL1_HUMAN
DOI=10.1038/sj/onc/1204740; Lalle P., Gouy M., Rigal D., sociates with Bcl-Xs and is an 1. Suppresses apoptosis induced by and BAX. Interacts with APAF-1. d with mitochondria and the nuclear essed in adult tissues. lungs, the liver and the kidneys. 2 family. mology 1 (BH1) domain. mology 2 (BH2) domain. It is produced through a collaboration informatics and the EMBL outstation - te. There are no restrictions on its slong as its content is in no way	OI=10.1093/hmg/10.21.2329; ember of the Bcl-2 family, blocks pathway but not in the death OI=10.1074/jbc.C000871200; that differentially binds and	194 AA. update) n update) e 10 protein) (Anti-apoptotic e 1, Vertebrata; Euteleostomi; hini; Hominidae; Homo.	Q9nr76 homo sapien P55269 homo sapien Q8cfr2 mus musculu Q9cyw5 mus musculu Q91827 xenopus lae Q925a9 rattus norv Q71560 rattus norv Q71560 rattus norv Q71540 rattus norv Q88996 rattus norv Q71540 rattus norv Q81945 canis famil P10415 homo sapien Q8uwd6 brachydanio Q91914 brachydanio Q91914 brachydanio Q8cg14 mus musculu Q07820 homo sapien

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30; GO:0005624; C:membrane fraction; TAS.
30; GO:0005615; F:protein binding; TAS.
GO; GO:0006916; P:anti-apoptosis; TAS.
GO; GO:0006915; P:apoptosis; TAS.
GO; GO:0006919; P:caspase activation; TAS.
GO; GO:0007292; P:female gamete generation; TAG.
GO; GO:0007293; P:spermatogenesis; TAS.
GO; GO:0007283; P:spermatogenesis; TAS.
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J. Neurochem. 85:1500-1512(2003).
EMBL; AY029163; AAK31792.1; -.
GO; GO:0042981; P:regulation of a
                                                                                             differentiation.
                                                                                                                                                STRAIN-Sprague-Dawley;
MEDLINE-22672518; PubMed-12787069;
Itoh T., Itoh A., Pleasure D.;
                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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01-JUN-2001
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InterPro; IPR002475; BCL2_family.
Pfam; PF00452; Bc1-2; 1.
SMART; SM00337; BCL; 1.
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EMBL; AF326964; AAK48715.1;
EMBL; AJ458330; CAD30221.1;
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PS01080; BH1; FALSE_NEG.
PS01258; BH2; 1.
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RESULT 3
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis regulator Bcl-B (Bcl-2-like 10 protein) (Anti-apoptotic protein Boo) (Bcl-2 homolog Diva).

Name=Bcl210; Synonyms=Boo, Diva;
Mus musculus (Mouse).
                                                                                                                                  STRAIN-C57BL/6 X DBA/2;
MEDLINE=99047617; PubMed=9829980; DOI=10.1074/jbc.273.49.32
Inohara N., Gourley T.S., Carrio R., Muniz M., Merino J., G
Koseki T., Hu Y., Chen S., Nunez G.;
"Diva, a Bcl-2 homologue that binds directly to Apaf-1 and BH3-independent cell death";
J. Biol. Chem. 273:32479-32486(1998).
-!- FUNCTION: Promotes cell survival. Suppresses apoptosis.
-!- SUBUNIT: Binds to Bcl-2, Bcl-X and BAX. Interacts with
-!- SUBCELLULAR LOCATION: Associated with mitochondria and
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C576IL/6 X DBA/2; TISSUE=Ovary;
MEDLINE=99094902; PubMed=9878060; DOI=10.1093/emboj/18.1.167;
Song Q.Z., Kuang Y.P., Dixit V.M., Vincenz C.;
Song Q.Z., Kuang Y.P., Dixit V.M., Vincenz C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002475; BCL2_family. Pfam; PF00452; BCl-2; 1. SMART; SM00337; BCL; 1.
                          This
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
              between
                                                                                                                                                                                                                                                                        SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCLB MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                 envelope (By similarity).

TISSUE SPECIFICITY: Expressed in multiple Restricted to the ovary and testis in adul SIMILARITY: Belongs to the Bcl-2 family.

SIMILARITY: Contains 1 Bcl-2 homology 1 (B SIMILARITY: Contains 1 Bcl-2 homology 2 (B
European
            SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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PS01258; BH2; 1.
185 AA; 21859 MW; 2E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MADPLRERTELLIADYLGYCAREPGTPEPAPSTPEAAVLRSAAARLRQIHRSFFSAYLGY
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ilarity 46.4%;
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 Institute.
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Pred. No. 1.5e-37;
5; Mismatches 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                    pDOI=10.1074/jbc.273.49.32479;
R., Muniz M., Merino J., Garci
G.;
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(BH2) domain.
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; Murinae; Mus
  restrictions
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Malek S., Carninci P., Prange C.,
Diatchen M.J., Wolferina D.K., Mullahy S.J.,
Diatchen M.J., Malek J.A., Gunaratne P.H.,
Diatchen M., Moley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Ullalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Diatchen M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Diatchen M.C.,
Diatchen C.M., Touchman J.W., Green E.D., Dickson M.C.,
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Best Local (
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GO; GO:0006916; P:anti-apoptosis;
GO; GO:0006915; P:apoptosis; IDA.
InterPro; IPR000712; Bc12 BH.
InterPro; IPR002475; BC12_family.
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Egg;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia;
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Last annotation updat
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Pred. No. 2.
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Q9E1F2;
01-MAR-2001
01-MAR-2001
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EMBL; BC052690; AAH52690.1; -.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0006916; P:anti-apoptosis; IDA.
GO; GO:0006916; P:apoptosis; IDA.
InterPro; IPR000712; Bc12 BH.
InterPro; IPR002475; BCL2_family.
SMART; SM00337; BCL1; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
SEQUENCE 191 AA; 22230 MW; F2F176E6B0DE69A6 CRC64;
                                                                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. RSORF1 N13-like protein.
  PROSITE;
                        InterPro; IPR000712; Bc12 BH.
InterPro; IPR002475; BC12 family.
Pfam; PF00452; Bc1-2; 1.
SMART; SM00337; BCL; 1.
                                                                                    EMBL; AF282130; AAG30102.1; HSSP; Q07817; 1R2I.
                                                                                                         "The genome of herpesvirus of turkeys: Marek's disease viruses.";
J. Gen. Virol. 82:1123-1135(2001).
                                                                                                                                                Kingham B.F.,
Schmidt C.J.;
                                                                                                                                                          MEDLINE=21195611; PubMed=11297687; Kingham B.F., Zelnik V., Kopacek J.,
                                                                                                                                                                                     STRAIN-FC12
                                                                                                                                                                                                                                              Meleagrid herpesvirus 1 (herpesvirus of turkeys).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                      Name=RSORF1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,0
"Generation and initial analysis of more than 15,0
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rodriguez A.C., Grimwood J.,
Krzywinski M.I., Skalska U.,
                                                                       GO; GO:0042981; P:regulation of apoptosis;
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                   NCBI_TaxID=37108;
                                                                                                                                                                                                                                 Alphaherpesvirinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPLRERTELLLADYLGYCAREPGTPEPAPSTPEAAVLRSAAARLRQIHRSFFSAYLGYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRLELVKQMADKLLSKDQDFSWSQLVMLLAFAGTLMNQGPYMAVKQKR---
                                                                                                                                                                                                                                                                                                                                                                                                           SGFFATAIFFIWKRL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                  SCLLTTAFIYLWIRL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRVIVTRDCCLIVNFLYNLLMGRRHRARLEALGGWDGFCRFFKNPLPLGFWRRLLIQAFL
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              PS50062;
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                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Egg;
  BH2; UNKNOWN
            BCL2_FAMILY; 1.
                                                                                                                                                                                                                                   Mardivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.18;
                                                                                                                                                                                                                                                                                            16,
26,
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                                                                                                                                                                                                                                                                                             Last
Last
                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 467.5; DE
Pred. No. 1e-35;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schmutz J., Myers R.M., Smailus D.E., Schnerch
                                                                                                                                                                                                                                                                                             sequence update) annotation updat
                                                                                                                                                            Majerciak V.,
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A., Schein J.
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RESULT 6
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                                                                            PROSITE;
PROSITE;
PROSITE;
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NR13_C
                                      Apoptosis;
                                                                                                                                HSSP; Q07817; 1MAZ.
InterPro; IPR000712; Bcl2 BH.
InterPro; IPR002475; BCL2 family.
Pfam; PF00452; Bcl-2; 1.
                                                                                                                                                                                          EMBL; X84418; CAA59136.1; -. HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rous sarcoma virus."
EMBO J. 14:1372-1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gillet G., Guerin M., Trembleau A., Brun G.;
"A Bcl-2-related gene is activated in avian cells transformed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q90343;
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    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fibroblast, and Neuroretina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95246730; PubMed=7729415;
                                                                                                                                                                                                                                                                                                                                                                                                     after embryonic day 7 in the optic tectum, and correl, onset of apoptosis in this area. SIMILARITY: Belongs to the Bcl-2 family. SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain. SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: Expression is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Plasma membrane. TISSUE SPECIFICITY: Mainly expressed in neural and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Rous sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    properties.
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                                                                                PS01258;
                                                                                                  PS01080;
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                                                                                                                    PS50062;
75 94
126 141
86 106
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                                                                                                                    FAMILY; 1.
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BH1.
BH2.
Potential.
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Pred. No. 2.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dramatically
                                                                                                                                                                                                                                                                                                         There are no restrictions ng as its content is in
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RESULT 8
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Query Match
Best Local Similarity
Matches 60; Conserv
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Best Local Similarity
Matches 57; Conserv
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Anti-apoptotic NR13.
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota, Metazoa, Neognathae, Galliformes, Phasianidae, Phasiani
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Q90ZN1;
01-DEC-2001
01-DEC-2001
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PROSITE;
Q9DH00 PRELIMINARY;
Q9DH00;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0042981; P:regulation Pfam; PF00452; Bcl-2; 1. SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=22304624; PubMed=12133006; DOI=10.1042/BJ20020836;
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                                                                                                                                                                                                                                                                                                          KKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQHRAWLQAQGGWDGFCHFF
                                                                                                                                                                                                                                                                                                                                                                                           ARAEPR-EAAALLRKVAAQLEAEGGLNWGRLLALVVFTGTLAAALAESGCEEGP--
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177 AA;
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33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.4%; Score 188.5; DB 2 34.9%; Pred. No. 1.3e-09; tive 12; Mismatches 57
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Pred. No. 4.5e.
6; Mismatches
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Q8UWD5;
01-MAR-2002
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InterPro; IPR002475; BCL2_family.
Pfam; PF00452; Bc1-2; 1.
SMART; SM00337; BCL; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
SEQUENCE 162 AA; 17286 MW; 97CE08A7834EA58B CRC64;
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"The genome of turkey herpsavirus.";
J. Virol. 75:971-978(2001).
HSSP; Q07817, 1R2I.
ZFIN; ZDB-GENE-030825-2; mclll
GO; GO:0042981; P:regulation o
Pfam; PF00452; Bc1-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish)
Bukaryota; Metazoa; Chordata;
Bukaryota; Metazoa; Chordata;
Carinataryoni; Neopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF291866; AAG45828.1; -.
EMBL; AF291866; AAG45819.1; -.
HSSP; Q07817; 1R2I.
G0; G0:0042991; P:regulation of apoptosis;
                                                                                                                                      Inohara N., Nunez G.;
Submitted (OCT-2001) to the
EMBL; AF441285; AAL32471.1;
                                                                                                                                                                                                                                                                                                                                               Inohara N., Nunez G.;
"Genes with homology
zebrafish.";
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20373792; PubMed=10917738; Inohara N., Nunez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=mclll; Synonyms=nrl3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meleagrid herpesvirus 1 (herpesvirus of turkeys).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to Apoptosis inhibitor, inhibitor-like protein).
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Last annotation update)
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tor, Bcl2 family proteins (Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 178.5;
Pred. No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Danio rerio).
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                                      apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                  apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOI=10.1128/JVI.75.2.971-978.2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEA.
                                                                                                                                                                                                                                                                                                                                                                              regulators identified
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                                                                                                                                                                            databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 11
Q9W6F1
ID Q9W6F
AC Q9W6F
DT 01-NC
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Q804D0
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Best Local
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Best Local (
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Q9W6F1;
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q804D0
Q804D0;
01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                Submitted (NOV-2002) to the EMBL/GenBank/DD EMBL; AY186728; AAO31808.1; -. HSSP; Q07817; 1MAZ. GO; GO:0042981; P:regulation of apoptosis; InterPro; IPR000712; BC12 BH. InterPro; IPR002475; BC12 family. Pfam; PF00452; BC1-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                            SMART; SM00337; BCL; 1.
PROSITE; PS50062; BCL2 FAMILY; 1.
SROUENCE 177 AA; 18891 MW; B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Gallus gallus (Chicken).
Finkarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, C
01-JUN-2003 (TrEMBLrel. 24, L
01-OCT-2003 (TrEMBLrel. 25, L
Bcl-2 related anti-apoptotic
                                     Q9W6F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=NR13
                                                                                                                                                                                                                                                                                                                                                                                                                         Neiman P.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00337; BCL;
                                                                                      110
                                                                                                                         119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 LRERTELLLADYLGYCAREPGTPEPAPSTPEAAVLRSAAARLRQIHRSFFSA----YLGY
                                                                                                                                                                                               \vdash
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                                                                                                                                                                                                                                                            Similarity
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PS01258; BH2; UNKNOWN_I.
176 AA; 19677 MW; 26CDE124AE77F573
                                                                                                                                                              GYPGNRFELVALM--ADSVLSDSPGPTWGRVVTLVTFAGTL------LERGPLVTARW
                                                                                                                                                                                                                     MADPLRERTELLLADYLGYCAREPGTPEPAPSTPEAAVLRSAAARLRQIHRSFF--SAYL
                                                                                                                       KKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQHRAWLQAQGGWDGFCHFF
                                                                                                                                                                                               MPGSLKEETALLLEDYFQH--RAGGAALPPSAT--AAELRRAAAELERRERPFFRSCAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WKKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQHRAWLQAQGGWDGFCHFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGNRFELVALMAD - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LREQTILLLAEDYISFCSGIQQTP-PSES---AEAMRYLAKEMEQQHRTKFRSLSQEFLDT
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ENSEGS-----RRLAETIADYLGGEKQDWLVENGGWEGFCRFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ADPSKCLQSVMRELVGDGKMNWGRVVSIFTFTGVLASELLSRG----
                                                                                                                                                                                                                                                         16.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.3%; Score 176.5; DB 2;
31.8%; Pred. No. 1.7e-08;
tive 21; Mismatches 46;
                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SVLSDSPGP---TWGRVVTLVTFAGT----LLERGPLVTAR
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                               Score 174.5; DB 2
Pred. No. 2.7e-08;
2; Mismatches 59
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                                                                                                 SRLAAALAAYLAEEQGEWLEEHARWDGFCRFF
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                                                                                                                                                                                                                                                                                                                                                                                                             databases
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                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                         177;
                                                                                                                                                                                                                                               43;
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                                                                                                                          170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143
                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                        118
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(TrEMBLrel. (TrEMBLrel.

12,

Last

sequence update)

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RESULT 12
Q8HYU
ID Q8HYU
AC Q8HYU
AC Q8HYU
DT 01-MA
DT 01-OC
DE BAX.
OS CAnias
OC Eukar
OC Mamma
OX NCBI
RN [1]
RN [1]
RN [1]
RP SEQUE
RA YAZAW
RL SUDMi
DR HSSP;
DR HSSP;
DR HSSP;
DR HSSP;
DR HSSP;
DR Inter
DR Inter
DR Pfam;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PP00452; Bc1-2; 1.

SMART; SM00337; BC1; 1.

PROSITE; PS50062; BCL2; PAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01080; BH2; UNKNOWN 1.

PROSITE; PS01158; BH2; UNKNOWN 1.

NON TER

NON TER

SEQÜENCE 211 AA; 23143 MW; A4B0
                                                                                                                                                                                                    Q8HYU5;
01-MAR-2003
01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myeloid cell leukemia protein MCL-1 (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata: Vartellarchosanria.
      Yazawa M., Masuda K., Ohno K., Tsujimoto H. Submitted (FEB-2002) to the EMBL/GenBank/DD EMBL, AB080230; BAC53619.1; -. HSSP; Q07812; 1F16.
GO; GO:0042981; P:regulation of apoptosis; InterPro; IPR000712; Bc12_BH.
InterPro; IPR0002475; BC12_family.
                                                                                                                                           Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sofer L., Burnside J.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF120210; AAD31644.1; -.
GO; GO:0042981; P:regulation of apoptosis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genes Dev. 13:718-728(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fabricius."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=99190706; PubMed=10090728;

Lee R.M., Gillet G., Burnside J., Thomas & Role of Nr13 in regulation of programmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archosauria;
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                 NCBI_TaxID=9615;
                                                                                                                                                                                                                                                          Q8HYU5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000712; Bcl2_BH.
InterPro; IPR002475; BCL2_family.
                                                                                                                                                                                                                                                                                                                           172
                                                                                                                                                                                                                                                                                                                                                    166
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                                                                                                                                                                                                                                                                                                                                                                                                        106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                    FCHFFR 171
                                                                                                                                                                                                                                                                                                                                                                                                        TLLERGPLVTARWKKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQHRAWLQAQGGWDG
                                                                                                                                                                                                                                                                                                                                                                                                                                  RVGDGVMQKHELAFQGMLRKLEIKKEDDLQAVCEVAAQVFND--GVTNWGRVVTLISF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                           QIHRSFFSAY-LGYPG-----NRFELVALMADSVLSDSPGPT-WGRVVTLVTFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DELRQESLELILRYLREAAGEAEPGVKKLFPGLLGGPGRPGRASS----AVMEKALETLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPLRERTELLLADYLGYCARE------PGTPEPAPSTPEAAVLRSAAARLR
                                                                                                                                                                                                                                                                                                                           FVDFFR
                                                                                                                                                                                                  (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     etazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               -GAFVAKHLKS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%;
                                                                                                                                                                                                    23,
23,
25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                  Last sequence update)
Last annotation updat
                                                                                                                                                                                                                             Created)
                                                                               C., Tsujimoto H.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 143.5;
Pred. No. 2.7
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                                                                                                                                                                                                                                                          PRT;
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ogrammed cell
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                                                                                                                                                                                                    update)
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                                                                                  databases
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death :
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                                                                                                                                                  Canis.
                                                                                                                                                              Euteleostomi;
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in
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Q8SQ43
ID Q8SQ4
AC Q8SQ4
AC Q8SQ4
DT 01-JU
DT 01
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Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB080724; BAB85810.1; -...
HSSP; Q07812; 1F16.
GO; GO:0042981; P:regulation of ap
InterPro; IPR000712; BC12_BH.
InterPro; IPR002475; BCL2_family.
Pfam; PF00452; BC1-2; 1.
SMART; SM00337; BCL: 1
PROSITE: DC12; 1.
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Best Local
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Q8SQ43;
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
Bax-protein.
                                                                                                                                                                                                                                                                                                                                               SMART; SM00337; BCL; 1
PROSITE; PS50062; BCL2
PROSITE; PS01080; BH1;
PROSITE; PS01080; BH2;
PROSITE; PS01259; BH3;
SEQUENCE 192 AA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9685;
                                             112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50062; BCL2
PS01080; BH1;
PS01258; BH2;
PS01259; BH3;
                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                 PS01258; BH2; 1.
PS01259; BH3; 1.
192 AA; 21283 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 PS50062; BCL2_FAMILY;
PS01080; BH1; 1.
                                                                                                                                                                                                                TMADPLRERTELLLADYLGYCAREPG--TPEPA-PSTPEAAVLRSAAARLRQIHRSFFSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSYFGTP----TW--QTVTIFVAGVL-TASLTIWKKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----PLVTARWKKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQHRAWLQAQGGWDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLGYPGNRFELVALMADSVLSDSPGP-----TWGRVVTLVTFAGTLLERG
                                                                                                                                                                            TSSEQIMKTGALLLQGFIQDRAGRMGGETPELALEQVPQDASTKKLSECLKRIGDELDS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHFFRTPFPLAFWRKQLVQAFLSCLLTTAFIYLWTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCTKVPELIRTIMGW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSSEQIMKTGALLLQGFIQDRAGRMGGETPELPLEQVPQDASTKKLSECLKRIGDELDS-
LCTKVPELIRTIMGW-
                                                                                      -----NMELQRMIA-AVDTDSPREVFFRVAAEMFSDGNFNWGRVVALFYFASKLVLKA
                                                                                                                                 YLGYPGNRFELVALMADSVLSDSPGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 AA;
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                                                                                                                                                                                                                                                                  Conservative
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                                           PLVTARWKKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQHRAWLQAQGGWDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21299 MW;
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                                                                                                                                                                                                                                                                                    11.6%;
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21,
24,
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Last sequ
Last anno
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                                                                                                                                                                                                                                                                Score 126; DB
Pred. No. 0.00
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R., Hasegawa A.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 131; DB Pred. No. 0.00 Pred. No. 0.00
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                                                                                                                                                                                                                                                                                                                                                      852D271AE86923FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis;
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0.001;
70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.00035;
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      TLDFLRERLLG
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                                                                                                                                                                                                                                                                                                        Length 192;
                                                                                                                                     --TWGRVVTLVTFAGTLLERG
                                                                                                                                                                                                                                                                  Indels
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                        ••
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                                                                                                                                                                                                                                                                  62;
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                                                                                                                                                                                                                                                                  Gaps
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         161
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LSYFGTP----TW--QTVTIFVAGVL-TASLAIWKKM 191

CHFFRTFFFLAFWRKQLVQAFLSCLLTTAFIYLWTRL

167

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RESULT 14
Q9W6F2
IDW Q9W6F
AC Q9W6F
DT 01-NC
DT 01-NC
DT 01-MC
OC GA11
OC GA11
OC GA11
OC GA11
OC GA1
OC GA
   RESULT 15
Q9JKL3
ID Q9JKL
AC Q9JKL
DT 01-OC
DT 01-JU
DE BAX P
OS Rattu
OC Eukar
OC Mamma
OX NCELL
RN [1]
RP SEQUE
RC TISSU
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Best Local Similarity
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Q9W6F2;
Q1-NOV-1999 (TrEMBLrel. 12,
Q1-NOV-1999 (TrEMBLrel. 12,
Q1-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sofer L., Burnside J.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF12021; AAD31645.1; -.
GO; GO:0042981; P:regulation of apoptosis; IEA.
InterPro; IPR000712; Bcl2 BH.
InterPro; IPR0002475; BCL2_family.
Pfam; PF00452; BCL2_; 1.
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                Q9JKL3 PRELIMINARY; PRT; 173 AA.
Q9JKL3;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
O1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Bax protein splice variant k.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50062; BCL2_FAMILY; 1.

PROSITE; PS01258; BH2; UNKNOWN_1.

SEQUENCE 174 AA; 20095 MW; 4880F463DB22B352 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein Al.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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MEDLINE=99190706; PubMed=10090728;
Lee R.M., Gillet G., Burnside J., Thomas S.J.,
Lee R.M., Gillet G., Burnside J., Thomas Cell

"Role of Nr13 in regulation of programmed cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
K., He X., Greenberg D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 VARDCQRLVALLSSRLMGQHRAWLQAQGGWD-GFCHFFRTPFPLAF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----MADSVLSD--SPGPT-WGRVVTLVTFAGTLLERGPLVTARWKKWGFQPRLKEQEGD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAKRIFNGVMEEKFADGNTNWGRIMTIFTFGG-----LLTKKLQEHGVQLTGEEKE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAQDYLQYVLQESHL-GPA-QTRVAHVLRNIASSLQDQTEEALRPFL----DRIDITSVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----KISYFITEYIINNKAAWIDANGGWENGFLTKFERRSPLSF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%; Score 125; DB 2; Length 17
27.1%; Pred. No. 0.0012;
tive 33; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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   Simon R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174
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      Graham S.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neiman P. death in
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PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
SEQUENCE 173 AA; 19661 MW; F1
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SMART; SM00337; BCL; 1.
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----TW--QTVTIFVAGVL-TASLTIWKKM 172
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Search completed: June 6, 2005, 10:43:39 Job time : 62 secs

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Result
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23 LADYLGYCAREPGTPE-PAPSTPEAAVLRSAAARLRQIHRSFFSAYLGYPGNRFELVALM 81

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Query Match Best Local Matches 5	RESULT 1 US-08-112-208C-3 J Sequence 3, Appli, patent No. 56917 GENERAL INFORMAT APPLICANT: KO, TITLE OF INVENVI NUMBER OF SEQUENCE ADDRESSES: STREET: 379 CITY: Palo, STATE: Cali. COUNTRY: US ZIP: 94301 COMPUTER READAL MEDIUM TYPE: COMPUTER: II OPERATING SY. SOFTWARE: PLICATION APPLICATION: PILING DATE: CLASSIPICATION TYPE: CLASSIPICATION: TELEGRANUS COMMUNICATION REFERENCE/DOMENTATION REFERENCE/DOMENTATION FOR: SEQUENCE CHARALLENGTH: 192 TYPE: amino STRANDEDNESS TOPOLOGY: 1 MOLECULE TYPE: MAME/KEY: PLOCATION: 1 LOCATION: INFORMATION: PORING STRANDEDNESS TOPOLOGY: 1 MOLECULE TYPE: FEATURE: FEATURE: FEATURE: PLOCATION: 1 LOCATION: 1 LOCATION: 1 LOCATION: DOMENTATION OTHER INFORMATION TO THE PLOCATION: 1 LOCATION: 1 LOCATION: 1 LOCATION: DOMENTATION OTHER INFORMATION TO THE PLOCATION: 1 LOCATION: 1 LOCATIO	,	28 11 30 11 31 32 31 33 31 33 31 33 31 33 31 33 31 34 34 34 34 34 34 34 34 34 34 34 34 34
Similarity 4; Conservat	C-3 Application Sofility FORMATION: T: KORSMEYER T: KORSMEYER T: KORSMEYER TINVENTION: F SEQUENCES: NDENCE ADDRES SEE: Townsen: 379 LYtton Palo Alto California Y: US 94301 READABLE FOR TYPE: Flopp ER: IBM PC G ING SYSTEM: RE: Patentin APPLICATION UMBER: DATE: 26-AU ATION NUMBER: LATION NUMBER: ONE: (415) 326 N FOR SEQ ID CHARACTERIST 192 amino amino acid EDNESS: Sing GY: Protein ON: 1.192 INFORMATION: C-3 C-3		22 1 1 1 0 0 0 8 8 8 1 1 0 0 0 9 9 1 1 0 0 0 8 8 8 1 1 0 0 0 1 1 1 1 1 1 1
11.2%; Score 26.7%; Pred. ive 22; Mis	112208 11ey J EATH TOWNS .e TOWNS .e #1 /MS-D .se #1 8/112 00N:	Þ	192 4 US-0 192 2 US-0 192 1 US-0 192 1 US-0 192 2 US-0 192 2 US-0 192 3 US-0 192 3 US-0 193 4 US-0 193 4 US-0 193 4 US-0 193 3 US-0 193 4 US-0 193 4 US-0 193 4 US-0 193 4 US-0 193 1 US-0
121; DB 1 No. 5.8e-0 smatches	ATORS hourie	ALIGNMENTS	US-08-927-326-2 US-08-112-208C-8 US-08-112-208C-8 US-08-248-819A-8 US-08-337-646A-8 US-08-856-034-8 US-08-856-034-8 US-08-9127-048-6 US-08-927-326-8 US-09-155-327G-7 US-09-155-327G-9 US-09-155-327G-9 US-09-155-327G-9 US-09-155-327G-10
; Length 19 6; 64; Indels	and Crew		δ.
2; 62; Gaps			Sequence 2, Sequence 2, Sequence 8, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 24, Sequence 6, S
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GENERAL INFORMATION:
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NFORMATION FOR SEQ ID NO: 3:
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APPLICATION NUMBER: US 01
APPLICATION SECTION: US 01
APPLICATION NUMBER: US 01
APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Smith, William M
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 25-NA: CLASSIFICATION: 43:
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LOCATION:
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ADSVLSDSPGP-----
                                                IQDRAGRMAGE--TPELTLEQPPQDASTKKLSECLRRIGDELDS-----NMELQRMI
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                                                                                                                                                                                                                                                                       /note= "Protein sequence of murine
Bax."
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-----TWGRVVTLVTFAGTLLERG-----PLVTARWKKW 121
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US-08-337-646A-3
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                                                                                                                                                                        Matches
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APPLICANT: KORSME
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                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                              NAME/KEY: Protein LOCATION: 1..192 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 25-MA
                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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STATE: California
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INFORMATION FOR SEQ ID NO:
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LENGTH: 192 amino acids
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PILING DATE: 26-ANG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 25-MAY-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 10-NOV-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                     23 LADYLGYCAREPGTPE-PAPSTPEAAVLRSAAARLRQIHRSFFSAYLGYPGNRFELVALM
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                                                              IQDRAGRMAGE--TPELTLEQPPQDASTKKLSECLRRIGDELDS-----NMELQRMI 80
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KORSMBYER, Standard CELL F
                                                                                                                                                  Conservative
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SYSTEM: PC-DOS/MS-DOS
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Bax."
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                                                                                                                                                Score 121; DB 2;
Pred. No. 5.8e-06;
2; Mismatches 64
----TWGRVVTLVTFAGTLLERG-----PLVTARWKKW 121
                                                                                                                                                  64;
                                                                                                                                                                                    Length 192;
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                                                                                                                                                  62;
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                                                                                                                                                                                                                                                                                  Query Match
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SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,53
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATIC
NAME: HOLLAND, Donald
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                  Local
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               182 QLVQAFLSCLLTTAFIYLWTRL 203
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                                                                                                                                                 82
                                                                                                                                                                                                                  23 LADYLGYCAREPGTPE-PAPSTPEAAVLRSAAARLRQIHRSFFSAYLGYPGNRFELVALM 81
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                                                                                                                                                    ADSVLSDSPGP-----
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                                                                                                                   AD-VDRDSPREVFFRVAADMFADGNFNWGRVVALFYFASKLVLKALCTKVPELIRTIMGW 139
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1..192
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                 ---TWGRVVTLVTFAGTLLERG----PLVTARWKKW 121
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                                                  WIQDQGGWEGLLSYFGTP----TW--
                                                                                                                                                                                                                                                   64; Indels
                                                                                                                                                                                                                                                                                Length 192;
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US-08-927-326-3
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Sequence 3, Application US/08927326 Patent No. 6184202 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08856034 Patent No. 5955595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNBY/AGENT INFORMATION:
NAME: HOLLAND, Donald R.
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkan
STREET: 7733 Forsyth Blvd.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KORSMEYER, TITLE OF INVENTION: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note= "Murine BAX polypeptide"
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
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733 Forsyth Blvd., Suite 1400
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26.7%;
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Pred. No. 5.8e-06;
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                                                                                                                                                                                     -WIQDQGGWEGLLSYFGTP----TW-- 170
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US-09-379-820A-3; Sequence 3, Application US/09379820A; Patent No. 6500626
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: CELL DEATH REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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les 54; Conservative
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OTHER INFORMATION: /note= "Protein sequence of OTHER INFORMATION: Bax."
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STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                   QLVQAFLSCLLTTAFIYLWTRL 203
                                                                                                                 QTVTIFVAGVL-TASLTIWKKM 191
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US-08-607-269-25
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Matches
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LENGTH: 192
TYPE: PRT
ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TITLE OF INVENTION: Cell Death Regulator
FILE REFERENCE: 6029-1314
CURRENT APPLICATION NUMBER: US/09/379,820A
CURRENT FILING DATE: 1997-08-24
PRIOR APPLICATION NUMBER: 08/856,034
PRIOR APPLICATION NUMBER: 08/856,034
PRIOR PILING DATE: 1997-05-14
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/226
PILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
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APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
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                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,269
                                                                                                                                                                                                                                                                                                                                                         ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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nes 54; Conserv
                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Diego
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No. 5702897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTVTIFVAGVL-TASLTIWKKM 191
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4370 La Jolla Village Drive, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                         US 08/226,876
                                                                                                                                                                                                                                                         US/08/607,269
                                                                                                                                                                                                                                                                                                     Version #1.25
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US-08-471-058-13
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GENERAL INFORMATION:
                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 192 amino acid
                                                                                                                         NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKST NUMBER: 2364
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                           SOPTWARE: FABLUM DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
APPLICATION NUMBER: US/08/471,058
                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/320,157
FILING DATE: 07-0CT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
08/320,157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304-1018
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING TITLE OF INVENTION: PROTEINS, DNA ENCODING THE TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kiefer, Michael APPLICANT: Barr, Philip J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                            TELEFAX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 755 PAG
CITY: Palo Alto
STATE: CA
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 CHFFRTPFPLAFWRKQLVQAFLSCLLTTAFIYLWTRL 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLGYPGNRFELVALMADSVLSDSPGP-----TWGRVVTLVTFAGTILLERG 111
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                                                192 amino acids
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               single
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Matches
                 Query Match
Best Local Similarity
   Matches
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Patent No. 5942490
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                                                                                                                                                                                                                                                 TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                 NAME/KEY: Protein LOCATION: 1..192 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                   NAME: HOLLAND, Donald REGISTRATION NUMBER: 3
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11.1%; Score 120; DB 2; 25.3%; Pred. No. 7.7e-06; tive 29; Mismatches 71
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                                                                                 /note= "Human BAX polypeptide"
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                                                                                                                                                                                                                                                                                                                               35, 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
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                                Length 192;
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   Indels 62;
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; NAME/KEY: Protein
; LOCATION: 1..192
; OTHER INFORMATION: /note= "Human BAX polypeptide"
US-08-856-034-9
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US-08-856-034-9
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NAME: HOLLAND, Donald R.
REGISTRATION NUMBER: 35,197
REPERENCE/DOCKET NUMBER: 9761
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-518
TELEPHONE: 314-727-6092
INFORMATION FOR SEQ. ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08856034
Patent No. 5955595
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J
                                                                                                                                                                                               Matches 55;
                                                                                                                                                                                                                                  Query Match
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ADDRESSEB: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                       67 YLGYPGNRFELVALMADSVLSDSPGP-----
-----PLVTARWKKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQHRAWLQAQGGWDGF 166
                                                                                                                        TSSEQIMKTGALLLQGFIQDRAGRMGGEAPELALDPVPQDASTKKLSECLKRIGDELDS-
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                                                    ----NMELQRMIA-AVDTDSPREVFFRVAADMFSDGNFNWGRVVALFYFASKLVLKA 124
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                                                                                                                                                                                                                                                                                                                                                                                                                           192 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                            11.1%; Score 120; DB 2; 25.3%; Pred. No. 7.7e-06;
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                                                                                                                                                                                           29; Mismatches
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                                                                                                                                                                                                                              Length 192;
                                                                                     -TWGRVVTLVTFAGTLLERG 111
                                                                                                                                                                                             Indels
                                                                                                                                                                                             62; Gaps
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Db Qy	B 8	B &	B 8	Query M Best Lo Matches	; INFORM ; SEQU ; LE ; TY ; TY ; TO US-08-471	TELE	; ATTO	; CL; ; PRIO ; AP	COMPU OPERA' SOFTW CURRENT APPLIT	COMP	SI	CORR AD	; TITLE	; FACULT NO. 1	$\alpha = \infty$	Dβ	<i>Q</i>
167 CHFFRTDFPLAFWRKQLVQAFLSCLLTTAFIYLMTRL 203	112PLVTARWKKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQHRAWLQAQGGWDGF 166	67 YLGYPGNRFELVALMADSVLSDSPGPTWGRVVTLVTFAGTLLERG 111	10 TMADPLRERTELLLADYLGYCAREPGTPEPA-PSTPEAAVLRSAARLRQIHRSFPSA 66	Match 11.1%; Score 120; DB 3; Length 192; Local Similarity 25.3%; Pred. No. 7.7e-06; Les 55; Conservative 29; Mismatches 71; Indels 62; Gaps 11;	INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENOTH: 192 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear 08-471-057-13	NCE/DOCKET NUMBER UNICATION INFORM ONE: (415) 813- X: (415) 494-07	ORMATION: SUSAN K. BER: 33,943	CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/320,157 FILING DATE: 07-0CT-1994	TER: IBM PC con TING SYSTEM: PC ARE: Patentin R APPLICATION DAT CATION NUMBER:	COUNTRY: USA ZIP: 94304-1018 COMPUTER READABLE FORM: MEDIIM TYPE: Flormy disk	alo Alto California	DENCE ADDRESS EE: MORRISON	TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF NUMBER OF SPOTEMORE. 22	INFORMATION: CANT: KIEFER, MICH	2 L-057-13 No. Application US/08471057	FGTPTWQTVTIF	167 CHFFRTPFPLAFWRKQLVQAFLSCLLTTAFIYLWTRL 203

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RESULT 14
US-08-470-865-13
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-127-048-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13,
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
APPLICANT: BARR, PHILIP J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/127,048
CURRENT FILING DATE: 1998-07-31
EARLIER APPLICATION NUMBER: 60/061,823
EARLIER FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Korsmeyer, Stanley J.

APPLICANT: Schlesinger, Paul H.

TITLE OF INVENTION: Method for Identifying Apoptosis Modulating Compounds
FILE REFERENCE: 6029-6052
                                                                                                                                                                                                                                                      STREET: ///
STREET: ///
CITY: Palo Alto
CITY: California
ATTORNEY/AGENT INFORMATION:
                                                                CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/470,865
                                                                                                                                                                                                                           COMPUTER
                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                    MAPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                APPLICATION NUMBER: US 0
FILING DATE: 07-OCT-1994
                                                                                                                                                                                                                                           ZIP:
                                                                                                       FILING DATE:
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                                                                                                  06-JUN-1995
 SUSAN K
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                                                                                                                                                                                                                                                                                                                                                               ENCODING
22
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25.3%; Pred. No. 7.7e-06;
25.3%; oo. Mismatches 71;
                                                 US 08/320,157
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US-09-155-327G-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent NO. 0777-18 Patent NO. 0777-18 PATENT INFORMATION: APPLICANT: AMEAD Operations Pty Ltd APPLICANT: AMEAD OPERATION: A NOVEL MAMMALIAN GENE, bcl-2, BEITITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING OF APOPTOSIS
                                                                                                                                                                                                                                                          Query Match
Best Local :
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/155,327G
CURRENT FILING DATE: 1999-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PN8: PRIOR FILING DATE: 1996-03-27
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
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LENGTH: 192 amino acids
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TELECOMMUNICATION INFORMATION:
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TOPOLOGY: lir
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ilarity 25.3%;
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Pred. No. 7.7e-06;
9; Mismatches 71
                                                                                                                                                                                                                                      Score 120; DB 4;
Pred. No. 7.7e-06;
9; Mismatches 71
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                                 -TLDFLRERLLG----WIQDQGGWDGL 161
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Search completed: June 6, 2005, 10:45:12 Job time: 43 secs 뮍 162 LSYFGTP----TW--QTVTIFVAGVL-TASLTIWKKM 191

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Result
No.
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Maximum
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
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328.5
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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US-09-912-599-7
US-09-764-847-800
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US-10-071-174-19
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US-10-196-793A-46
US-10-101-482-13
US-10-277-693A-9
US-10-2878-5
US-10-2878-5
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US-09-033-525-2
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                                      Sequence 2, Appli
Sequence 7, Appli
Sequence 800, App
Sequence 800, App
Sequence 19, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 10, Appli
Sequence 10, Appli
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10.1	10.1	•	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.2	10.2	10.2	10.2	10.3	10.4	10.5	10.6	10.6	10.6	10.6	10.8	10.8	10.8	10.8	10.8		10.9
239	239	239	239	239	239	239	239	239	239	239	239	239	239	152	239	192	21	237	18	21	365	365	365	193	193	193	192	192	192	192	23
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US-10-148-953A-4	US-10-148-953A-2	US-10-148-953A-1	US-10-003-632C-13	US-10-003-632C-10	-632C-	US-10-003-632C-1		US-10-053-645A-21	US-10-141-618-12	US-10-277-693A-10	US-09-993-420A-8	US-08-726-211-5	US-10-148-953A-3		٠	US-10-277-693A-3	- 1			US-10-071-174-6	US-10-164-861-696	US-09-882-171-696	US-09-809-391-696	US-09-925-674A-9	US-10-450-366-6	US-09-925-674A-7	US-10-451-467A-2	US-10-421-285-8	US-10-277-693A-8	US-10-277-693A-2	US-09-912-599-14
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ALIGNMENTS

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; ORGANISM: Homo s
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APPLICANT: KE, NING
APPLICANT: GODZIK, ADAM
TITLE OF INVENTION: APOPTOSIS MODULATOR BCL-B AND METHODS FOR MAKING AND
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 087102-0272558
CURRENT APPLICATION NUMBER: US/10/071,174
CURRENT PILING DATE: 2002-02-07
PRIOR FILLING DATE: 2001-02-07
PRIOR FILLING DATE: 2001-02-07
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Best Local Similarity
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                           Matches 204;
121 WGFQPRLKEQEGDVARDCQRLVALLSSRLMGQHRAWLQAQGGWDGFCHFFRTPFPLAFWR 180
                                                                                       61
                                            61 RSFFSAYLGYPGNRFELVALMADSVLSDSPGPTWGRVVTLVTFAGTLLERGPLVTARWKK
                                                                                                                                                         1 MVDQLRERTIMADPLRERTELLLADYLGYCAREPGTPBPAPSTPBAAVLRSAAARLRQIH
                                                                      RSFFSAYLGYPGNRFELVALMADSVLSDSPGPTWGRVVTLVTFAGTLLERGPLVTARWKK 120
                                                                                                                                      MVDQLRERTIMADPLRERTELLLADYLGYCAREPGTPEPAPSTPEAAVLRSAAARLRQIH
                                                                                                                                                                                                                           100.0%; Score 1084; DB 14; ilarity 100.0%; Pred. No. 6.1e-103; Conservative 0; Mismatches 0;
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US-09-912-599-7
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Best Local S
Matches 130
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Patent No. US20020137767A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, P.
FILE REFERENCE: PC009
                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 800
LENGTH: 141
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SEQ ID NO 7
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APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: Bcl-2-like Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PT044P1
CURRENT APPLICATION NUMBER: US/09/912,599
CURRENT FILING DATE: 2001-07-26
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TYPE: PRT
ORGANISM: Homo sapiens
-09-912-599-7
               NAME/KEY: SITE
LOCATION: (6)
OTHER INFORMATION: 1
NAME/KEY: SITE
LOCATION: (7)
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 2003
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PRIOR APPLICATION NUMBER: PCT/US01/03080
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/179,487
                                                                                                 TYPE: PRT ORGANISM: FEATURE:
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NUMBER OF SEQ ID NOS: 15
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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mes 130; Conservative
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                                                   Xaa
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                                                  L-amino
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                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-C
NUMBER OF SEQ ID NOS: 2003
Prior Application removed -
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 800
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 800, Application US/10092154
Publication No. US20030054375A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
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NAME/KEY: misc_feature
LOCATION: (6)
OTHER INFORMATION: Xaa eo
NAME/KEY: misc_feature
LOCATION: (7)
OTHER INFORMATION: Xaa eo
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LOCATION: (9)
OTHER INFORMATION: X
NAME/KEY: SITE
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OTHER INFORMATION:
    OTHER INFORMATION:
                          LOCATION: (86)
OTHER INFORMATION: Xaa
NAME/KEY: misc_feature
                                                       NAME/KEY: misc feature
                                                                                                        LOCATION: (10)
OTHER INFORMATION: Xaa
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                          LENGTH: 141
TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (18)
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Xaa equals any of
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    occurring L-amino acids
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Query Match Best Local Similarity

30.3%; 67.0%;

Score 328.5; DB 14; Pred. No. 1.5e-25;

Length 141;

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US-10-071-174-13
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US-10-071-174-19
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LENGTH: 30
TYPE: PRT
                                                                  Query Match
Best Local S
Matches 24
                                                                                                                                                                       APPLICANT: GODZIK, ADAM
TITLE OF INVENTION: APOPTOSIS MODULATOR BCL-B AND METHODS FOR MAKING AND
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 087102-0272558
CURRENT APPLICATION NUMBER: US/10/071,174
CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/267,166
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PACENTIN Ver. 2.1
SEQ ID NO 13
LENGTH: 24
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/100 Publication No. US20030176671A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/10071174
Publication No. US20030176671A1
GENERAL INFORMATION:
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APPLICANT: KE, NING
APPLICANT: KE, NING
APPLICANT: GODZIK, ADAM
TITLE OF INVENTION: APOPTOSIS MODULATOR BCL-B AND METHODS FOR MAKING AND
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 087102-0272558
CURRENT APPLICATION NUMBER: US/10/071,174
CURRENT FILING DATE: 2002-02-07
DEFICE APPLICATION NUMBER: 2002-02-07
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: REED, JOHN APPLICANT: KE, NING APPLICANT: GODZIK, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/267,166
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                  15 LRERTELLLADYLGYCAREPGTPE 38
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                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         JOHN C.
                                                                                   11.8%; Score 128; DB 14; 100.0%; Pred. No. 6.6e-06;
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RESULT 8
US-10-101-482-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.2%; Score 121; DB 14; Best Local Similarity 27.4%; Pred. No. 0.00045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 46
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PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/332,886
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 60/306,091
PRIOR FILING DATE: 2001-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: THERAPEUTIC AGENTS COMPRISING PRO-APOPTOTIC PROTEINS FILE REPERENCE: CLFR: 0.12US CURRENT APPLICATION NUMBER: US/10/196,793A CURRENT FILING DATE: 2002-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ROSENBLUM, MARTIN G. APPLICANT: LIU, YUYING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-07-17 NUMBER OF SEQ ID NOS: 61
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDLIM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vei

CURRENT APPLICATION NUMBER: US/10/101,482

FILING DATE: 18-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KIEFER, MICHAEL C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 TPFPLAFWRKQLVQAFLSCLLTTAFIYLWTRL 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLGYPGNRFELVALMADSVLSDSPGP-----
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                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                ADDRESSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road
                                                                                                                                                                                                                          COUNTRY: USA
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                                                                             Version #1.30
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                                                                           Matches
                                                                                                                                                                                                                                   SEQ ID NO 9
                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/277,693A
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: 09/379,820
PRIOR FILING DATE: 1999-08-24
PRIOR PILING DATE: 1999-08-24
PRIOR PILING DATE: 1993-08-26
PRIOR PILING DATE: 1993-08-26
PRIOR APPLICATION NUMBER: 08/856,034
                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1997-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Cell Death Agonists FILE REFERENCE: 56029/36280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Korsmeyer, Stanley J.
                                                                                                                                                                       TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             LENGTH: 192
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                                                                                           Local Similarity
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/08/320,157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 LSYFGTP----TW--QTVTIFVAGVL-TASLTIWKKM 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 CHFFRTPFPLAFWRKQLVQAFLSCLLTTAFIYLWTRL 203
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TSSEQIMKTGALLLQGFIQDRAGRMGGEAPELALDPVPQDASTKKLSECLKRIGDELDS-
                                   TMADPLRERTELLLADYLGYCAREPG--TPEPA-PSTPEAAVLRSAAARLRQIHRSFFSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 813-5600
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                                                                                                                                                                                                                                                     version 3.1
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25.3%;
                                                                       11.1%; Score 120; DB 14; 25.3%; Pred. No. 0.00057; tive 29; Mismatches 71;
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Pred. No. 0.00057
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US-10-421-285-10
; Sequence 10, Application US/10421285
; Publication No. US20040053836A1
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FILE REFERENCE: MSK.P-053
CURRENT APPLICATION NUMBER: US/10/421,285
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: US 60/375,250
PRIOR FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 15
                                                                                                                         APPLICANT: MayerKuckuk, Phillip
APPLICANT: Banerjee, Debabrata
APPLICANT: Bertino, Joseph R.
TITLE OF INVENTION: Method for Modulating the
TITLE OF INVENTION: Vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/306,878
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: US 60/334,149
PRIOR FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, John C.
APPLICANT: Guo, Bin
TITLE OF INVENTION: Methods for Identifying Modulators of
TITLE OF INVENTION: Apoptosis
FILE REFERENCE: P-LJ 5535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 55; Conserv
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ACAT, Yehudith

APPLICANT: Ageilan, Rami
APPLICANT: Belotestotsky, Ruth
APPLICANT: Lorberboum-Galski, Haya
TITLE OF INVENTION: CHIMERIC PROTEINS WITH CELL-TARGETING
TITLE OF INVENTION: SPECIFICITY AND APOPTOSIS-INDUCING ACTIVITIES
FILE REFERENCE: 9457-009-999
CURRENT APPLICATION NUMBER: US/09/033,525
CURRENT FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSFO
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LENGTH: 331
TYPE: PRT
GRGANISM: Homo sapiens
US-09-033-525-2
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US-09-033-525-2
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Matches
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Best Local Similarity
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ORGANISM: human
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                                                                                                                                                                                                                                                                                                                        Local
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301
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LSYFGTP----TW--QTVTIFVAGVL-TASLTIWKKM 330
                                                                                                                                                                                       YLGYPGNRFELVALMADSVLSDSPGP------TWGRVVTLVTFAGTLLERG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LCTKVPELIRTIMGW-------TLDFLRERLLG----WIQDQGGWDGL 161
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                                 CHEFRTPFPLAFWRKQLVQAFLSCLLTTAFIYLWTRL 203
                                                                         LCTKVPELIRTIMGW-----WIQDQGGWDGL
                                                                                                                                                   ----NMELQRMIA-AVDTDSPREVFFRVAADMFSDGNFNWGRVVALFYFASKLVLKA 263
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                                                                                                           ----PLVTARWKKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQHRAWLQAQGGWDGF 166
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Pred. No. 0.00057;
29; Mismatches 71;
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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-912-599-14
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Publication No. US20050079154A1
GENERAL INFORMATION:
APPLICANT: Yarkoni, Shai
APPLICANT: Ben-Yehudah, Ahmi
Query Match
Best Local Similarity
                                                                                                                                     SEQ ID NO 14
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09912599
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. US20020106731A1
                                                                                                                                                                                PRIOR FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/912,599
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: PCT/US01/03080
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/179,487
PRIOR APPLICATION NUMBER: 60/180,697
PRIOR APPLICATION NUMBER: 60/180,697
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Bcl-2-like Polynucleotides, FILE REFERENCE: PT044P1
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PRIOR FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 10
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CURRENT APPLICATION NUMBER: US/10/640,668
CURRENT FILING DATE: 2003-08-13
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APPLICANT: Belotstotsky, Ruth
APPLICANT: Lorberboum-Galski, Haya
APPLICANT: Lorberboum-Galski, Haya
TITLE OF INVENTION: CHIMEBIC PROTEINS WITH CELL-TARGETING
TITLE OF INVENTION: SPECIFICITY AND APOPTOSIS-INDUCING ACTIVITIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ruben et al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSSEQIMKTGALLLQGFIQDRAGRMGGEAPELALDPVPQDASTKKLSECLKRIGDELDS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHEFRIPEPLAFWRKQLVQAFLSCLLTTAFIYLWTRL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----PLVTARWKKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQHRAWLQAQGGWDGF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NMELQRMIA-AVDTDSPREVFFRVAADMFSDGNFNWGRVVALFYFASKLVLKA 263
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    10.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----WIQDQGGWDGL 300
    Score 118; DB 9;
Pred. No. 6.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptides, and Antibodies
                            Length 23;
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Sequence 2, Application US/10277693A; Sequence 2, Application US/10277693A; Publication No. US20030096367A1; GENERAL INFORMATION:

APPLICANT: KOYEMEYEY, Stanley J.

TITLE OF INVENTION: Cell Death Agonists
FILE REFERENCE: 56029/36280

CURRENT APPLICATION NUMBER: US/10/277,693A; CURRENT FILING DATE: 2002-10-22; PRIOR APPLICATION NUMBER: 09/379,820; PRIOR PRILING DATE: 1999-08-24; PRIOR APPLICATION NUMBER: 08/112,208; PRIOR APPLICATION NUMBER: 08/856,034; PRIOR APPLICATION NUMBER: 08/856,034; PRIOR APPLICATION NUMBER: 08/856,034; PRIOR FILING DATE: 1997-05-14; NUMBER OF SEQ ID NO 2; SOFTWARE: PatentIn version 3.1; SEQ ID NO 2; TYPE: PATENTIAN SEPERANTSN: Homo sapiens
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Search completed: June Job time : 54 secs
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US-10-277-693A-2
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.9%; Score 118; DB 14; Length 192; Best Local Similarity 25.3%; Pred. No. 0.00092; Matches 55; Conservative 28; Mismatches 72; Indels 62; Gaps
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                                                                                                                                                        125 LCTKVPELIRTIMGW---
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                                                                                                                                                                                                                                                                                                               14 TSSEQIMKTGALLLQGFIQDRAGRMGGEAPELALDPVPQDASTKKLSECLKRIGDELDS- 72
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                                                                                                                                                                                                                               -----NMELQRMIA-AVDRDSPREVFFRVAADMFSDGNFNWGRVVALFYFASKLVLKA 124
                6, 2005, 10:46:10
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OM protein - protein search, using sw model
                                                      Run on:
June 6, 2005, 10:37:59; Search time 39 Seconds (without alignments)
. 503.288 Million cell updates/sec
                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Title: Perfect score: Sequence: 1 MVDQLRERTTMADPLRERTE.....QAFLSCLLTTAFIYLWTRLL 204 US-10-071-174A-2 1084

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

;	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	v	4	ω	N	1		Result
i	B	82.5	83	84	84.5	85.5	91	94	94.5	95	95.5	95.5	98	98.5	99.5	99.5	99.5	99.5	100.5	101.5	101.5	101.5	105.5	108	109	113	120	123	193.5	00010	
;	7.6	7.6		7.7	7.8	7.9	8.4	8.7	8.7	8.8	8.8	8.8	9.0	9.1	9.2	9.2	9.2	9.2	9.3	9.4	9.4	9.4	9.7	10.0	10.1	10.4	11.1	11.3	17.9	March	
	190	658	272	216	192	380	199	232	233	236	255	205	227	214	236	233	233	233	233	236	236	172	133	350	239	143	192	192	177	Terracti	
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	A47537	T46359	T35231	B37332	AI0268	A75500	TVMSB1	S24390	167431	TVMSA1	JC7567	TVHUB1	JE0203	149057	153744	S51761	I49056	B47537	A37332	167432	JC7383	I49449	I53295	A47476	TVHUA1	138921	A47538	D47538	S54778		;
1 m m m m m m m m m m m m m m m m m m m	a	-	hypothetical prote	_	anthranilate synth			transforming prote		transforming prote	Mcl-la protein - z	transforming prote	apoptosis regulato	bcl-x transmembran	gene bcl-2 protein	BCL-X protein - ra	bcl-x long - mouse	apoptosis regulato	transforming prote	BCL-2 - rat (fragm	B-cell lymphoma 2	hemopoietic-specif	bcl-2-associated p	BCL2 homolog MCL1	prot	bcl-2-associated p	bcl-2-associated p	ted	NR-13 protein - qu	11010410410404	

45	44	43	42	41	40	9	38	37	36	35	34	ω ω	32	31	30
76.5	76.5	77	77	77	78	78	78	78	78.5	79.5	80	80.5	81	81.5	82
7.1	7.1	7.1	7.1	7.1	7.2	7.2	7.2	7.2	7.2	7.3	7.4	7.4	7.5	7.5	7.6
386	354	543	462	365	1632	535	515	218	200	522	209	179	915	175	334
N	N	N	N	N	N	N	N	N	۔	μ	ν	N	N	N	N,
T36169	E87635	T34681	H70593	T34759	C70752	T37508	H75579	B47538	NNEB2D	S01927	E82241	JC7255	T09575	I39055	T17213
hypothetical prote	efflux system prot	probable secreted	hypothetical prote	oligopeptide ABC t	probable ctpI prot	hypothetical prote	hypothetical prote	bcl-2-associated p	anthranilate synth	nif-specific regul	preprotein translo	Bax-delta protein	smoothelin - human	Bcl-2 related - hu	hypothetical prote

ALIGNMENTS

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bcl-2-associated protein x, delta splice N;Alternate names: BAX; programmed cell c C;Species: Homo sapiens (man)
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C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; blocked amino end; het
E;172-191/Domain: transmembrane #status predicted <TMMI:
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A47538
   C;Date:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-192 <OLT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Bcl-2 heterodimerizes in vivo with a conserved A; Reference number: A47538; MUID:93364978; PMID:8358790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: A47538
R;Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: BAX; programmed cell death membrane protein > C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bcl-2-associated protein x, alpha splice form - human N,Alternate names: BAX; programmed cell death membrane protein x alpha
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Best Local S
Matches 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AD-VDTDSPREVFFRVAADMFADGNENWGRVVALFYFASKLVLKALCTKVPELIRTIMGW
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#sequence_revision 09-Mar-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.1%; Score 120; DB 2; I
25.3%; Pred. No. 0.00035;
ative 29; Mismatches 71;
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                                   e form - human
death membrane
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blocked
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                                       protein x delta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
   09-Jul-2004
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C;Species: Homo sapiens (man)
C;Jate: 31-Dec-1988 #sequence revision 07-Jun-1996 #text change
C;Jate: 31-Dec-1988 #sequence revision 07-Jun-1996 #text change
C;Jaccession: C37332; A29409; S02452; A24428; A27622; B27622
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gen
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: C37332
                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-95, 'A', 97-109, 'G', 111-236, 'S', 238-239 <TSU>
A; Residues: 1-95, 'A', 97-109, 'G', 111-236; PIDN: AAAS1813.1; PID: 9179367
A; Cross-references: GB: M13994; NID: 9179366; PIDN: AAAS1813.1; PID: 9179367
A; Note: this sequence has been corrected in reference A37332
A; Note: this sequence has been corrected in reference A37332
R; Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldm.
EMBO J. 7, 123-131, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P10415
A;Note: this report is a correction
R;Tsujimoto, Y; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A;Title: Analysis of the structure, transcripts, and protein
A;Reference number: A29409, MUID:86259760; PMID:3523487
A;Accession: A29409
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Genomics 26, 592-594, 1995
A;Title: Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and isolation A;Reference number: 138921; MUID:95331797; PMID:7607685
                       A; Molecule type: mRNA
A; Residues: 1-58, 'T',
                                                                                        R;Cleary, M.L.; Smith, S.D.; Sklar, J.
Cell 47, 19-28, 1986
A;Title: Cloning and structural analysis of cDNAs for bcl-2
A;Reference number: A24428; MUID:87002488; PMID:2875799
                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-239 <SET>
                                                                                                                                                                                                                               A; Reference number: S02452;
A; Accession: S02452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not A; Molecule type: DNA
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C; Superfamily: bcl
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A;Map position: 19q13.3-19q13.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:BAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic
A;Molecule type: mRNA
A;Residues: 1-143 <RES>
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                                                                   A; Accession: A24428
                                                                                                                                                                                                                                                                              A; Title: Alternative promoters and exons,
  A;Cross-references: GB:M14745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGDVARDCQRLVALLSSRLMGQHRAWLQAQGGWDGFCHFFRTPFPLAFWRKQLVQAFLSC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELVALMADSVLSDSPGPTWGRVVTLVTFAGTLLERG-----PLVTARWKKWGFQPRLKEQ 130
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,60-116,'R',118-239 <CLB>
GB:M14745; NID:g179370; P
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                                                                                                                                                                                                                                                         MUID:88196071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulator, inhibitory type
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Pred. No. 0.0012;
7; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shown;
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                                                                                                                                                                                                                                                                                 somatic mutation
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    PIDN: AAA35591.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 143
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  PID:g179371
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                                                                                                                     hybrid bcl-2/immunoglo
                                                                                                                                                                                                                                                                                                                              Goldman,
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A;Title: MCL1, a gene expressed in programmed myeloid cell differentiation, A;Reference number: A47476; MUID:93234528; PMID:7682708
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A;Map position: 18q21.3-18q21.3
C;Function:
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A;Residues: 1-6,'S',8-58,'T',60-128,'C',130-239 <HUA2>
A;Note: the sequence was determined from the germline gene
C;Comment: Constitutive expression of BCL2 following t(14:18)
                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: ML-1 myeloid cell leukemia
A;Note: sequence extracted from NCBI backbone (NCBIP:129734)
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A;Residues: 1-350 <KOZ>
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A; Residues: 1-58, 'T', 60-239 < HUA>
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A;Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: A;Reference number: A27622; MUID:88217344; PMID:3285301
A;Accession: A27622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Species: Homo sapiens (man)
;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
;Accession: A47476
                                                                                                                                                                                                                                               Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                   sequence extracted from Nords: transmembrane protein
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                                                 192
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                                                                                                                                                                                          13 DPLRERTELL-LADYLGYCAREPGTPEPAPSTP-----
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                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                Similarity
                                               GAKDTKPMGRSGATSRKALETLRRVGDGVQRNHETVFQGMLRKLDIKNEDDVKSLSRVMI
                                                                                                                                           EPLGKRPAVLPLLELVGESGNNTSTDGSLPSTPPPAEEEEDELYRQSLEIISRYLREQAT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AARLRQIHRSFFSAYLGYPGNRFELVALMADSVLSDSPGPTWGRVVTLVTFAGT
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LSDSPGPT-WGRVVTLVTFAGTLLERGPLVTARWKKWGFQPRLKEQEGDVARDCQRLVAL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGGWDAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYRRDFAEMSSQLHLTPFTA----RGRF---ATVVEELFRD--GVNWGRIVAFFEFGGV
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                                                                                              --EAAVLRSAAARLRQI------HRSFFSAYLGYPG--NRFELVALMADSV
                                                                                                                                                                                                                                     10.0%; Score 108; DB 2; 23.8%; Pred. No. 0.01; tive 20; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.1%; Score 109; DB 1; Length 239; 23.5%; Pred. No. 0.0052;
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
C;Accession: 149449
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J. Immunol. 151, 1979-1988, 1993
A;Title: Characterization of A1, a novel hemopoietic-specific
A;Reference number: 149449; MUID:93346743; PMID:8345191
A;Accession: 149449
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N;Alternate names: BAX; programmed cell death membrane protein x
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q07440; GB:L16462; NID:g293273; PIDN:AAA16886.1; PID:g293274
                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-172 < RES>
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A; Residues: 1-133 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Expression of members of the bcl-2 gene family in onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid A;Reference number: I53295; MUID:95129487; PMID:7828536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology 136, 232-241, 1995
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                                                                                                                                                                        Matches
                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 9.7%;
Local Similarity 27.2%;
                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 RLVALLSSRLMG-----QHR--AWLQAQGGWDGFCHFFRTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 ITDVLVRTKRDWLVKQRGWDGFVEFF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252
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                                                                                                                             22 LLADYLGYCAREPGTPEPAPSTPEAAVLRSAAARLRQIHRSFFSAYLGYPGNRFELVALM 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44;
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                                                                                                                                                                                               Similarity
                                         ADSVLS---DSPGPTWGRVVTLVTFAGTLLERGPLVTARWKKWGFQPRLKEQEGDVARD- 137
FNQVMEKEFEDGIINWGRIVTIFAFGGVLLKKLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HVFSDGVTNWGRIVTLISF-----GAFVAKHLK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRVAADMFADGNFNWGRVVALFYFASKLV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TWGRVVTLVTFAGTLLERGPLVTARWKKWGFQPRLKEQEGDVARDCQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPELTLEQPPQDASTKKLSECLRRIGDEL------DNNMELQRMIAD-VDTDSPREVF 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPE-PAPSTPEAAVLRSAAARLRQIHRSFFSAYLGYPGNRFELVALMADSVLSDSPGP--
                                                                                  LAEHYLQYVLQVPAF-ESAPSQACRVLQRVAFSVQKEVEKNLKSYLDDFHVESIDTARII
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                                                                                                                                                                        Conservative
                                                                                                                                                                                          9.4%; Score 101.5; DB 23.6%; Pred. No. 0.019;
                                                                                                                                                                      31;
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                                                                                                                                                                                                                                                                                                                            from GB/EMBL/DDBJ
                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                    172;
                                                                                                                                                                                                                                                                                                                                                                                          early-response
                                                                                                                                                                        29;
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-IALDV 112
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R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; DOILLBOUL, A.C.. Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid A;Reference number: I53295; MUID:95129487; PMID:7828536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
JC7383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 275, 899-903, 2000 A; Title: Cloning and functional analysis of cDNA encoding
                                                                                                                                                                                                                                                                                                     A; Residues: 1-236 < RES>
                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: I67432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCL-2
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                                                                                                                                                                                                                                                                                                                                                            A;Accession: I67432
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;Keywords: B-cell
                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                      Cross-references: UNIPROT:P49950; EMBL:U34964; NID:g1004378; PIDN:AAA77687.1; PID:g100 Superfamily: bcl apoptosis regulator, inhibitory type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                    RDFAEMSSQLHLTPFTA-----RGRF---ATVVEELFRD--GVNWGRIVAFFEFGGVMCV 156
                                                                                                                            RSAAARLRQIHRSFFSAYLGYPGNRFELVALMADSVLSDSPGPTWGRVVTLVTFAGTLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WDGFCHFFRTPF-PLAFWRKQLVQAFLSCLLTTAFIYLWTRL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESVNREMSPLVDN --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ERGPLVTARWKKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQH-RAWLQAQGG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŔDFĂEMSSQLHLTPFTĂ-----RGŘF---ĂTVVEELFRĎ--GVNWGRIVAFFEFGGVMCV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSAAARLRQIHRSFFSAYLGYPGNRFELVALMADSVLSDSPGPTWGRVVTLVTFAGTLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAYKQVSSFVAEFIMNNTGEWIRQNGGWEDGFIKKFE---PKSGW
  ESVNREMYPLVDN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WDAFVELYGPSVRPLFDFSWLSLKTLLSLALVGACITLGTYL
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                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis regulator, lymphoma; ovary
                                        ERGPLVTARWKKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQH-RAWLQAQGG 162
                                                                                                                                                                                          9.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.4%; Score 101.5; DB 25.3%; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                    17;
                                                                                                                                                                                          Score 101.5; DB Pred. No. 0.027;
                                                                                                                                                                      Mismatches
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17-Nov-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitory type
                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----IALWMTEYLNRHLHTWIQDNGG
                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61; Indels
  - IALWMTEYLNRHLHTWIQDNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                Length
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                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    supports cell survival.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the hamster Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                             the immature rat ovary: levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154
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                                                                                                                                                                      43;
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                                                                                                                                                                      Gaps
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  191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
B47537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: A37332; S35453
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Tsolation and characterization of the chicken bcl-2
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: A37332
                                                                                                                                                                                                                                                        A,Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of A,Reference number: A47537; MUID:93364977; PMID:8358789
A,Recession: B47537
A,Recession: B47537
A,Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                     N;Contains: apoptosis regulator bcl-xS
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: B47537; C47537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transforming protein (bcl-2-alpha) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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A;Cross-references: GDB:228079
C;Superfamily: bcl apoptosis r
                                                                                    A;Molecule type: mRNA
A;Residues: 1-69,'G',71-125,189-233 <BO2>
A;Cross-references: GB:L20122; NID:g623236;
                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-233 <BOI>
A;Cross-references: UNIPROT:Q07817; GB:L20121; NID:g510900; PIDN:CAA80661.1;
A;Accession: C47537
                                                                                                                                                                                                                                                                                                                                           R;Boise, I.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, Cell 74, 597-608, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apoptosis regulator bcl-xL - human N; Alternate names: bcl-2-related p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 189/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT: Q00709; EMBL: D11381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-233 <EGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A37332
                                          A;Gene: GDB:BCL2L
                                                                  ;Genetics:
                                                                                                                                                  Status: nucleic acid sequence not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 DEFSRRYQRDFAQMSGQLHLTPFTAH-----GRFVAV---VEELFRD--GVNWGRIVAFF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 REPGTPEPAPSTPEAAVLR-----SAAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFGGVMCVESVNREMSPLVDN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPPVPPAPAPAAPAAVAAAGASSHHRPEPPGSAAASEVPPAEGLRPAPPGVHLALRQAG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WDAFVELYGPSMRPLFDFSWQSLKTLLSLALVGACITL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WDGFCHFFRTPF-PLAFWRKQLVQAFLSCLLTTAFIYL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AWLQAQGGWDGFCHFFRTPF-PLAFWRKQLVQAFLSCLLTTAFIYL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFAGTLL-----ERGPLVTARWKKWGFQPRLKEQEGDVARDCQRLVALLSSRLMGQH-R 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NWIODNGGWDAFVELYGNSMRPLFDFSWISLKTILSLVLVGACITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
  apoptosis regulator, inhibitory type
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22.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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    chicken

                                                                                                                                                    shown;
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                                                                                        PIDN:CAA80662.1; PID:g623237
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                                                                                                                                                                                                                                                                                                                                                                     L.; Lindsten, T.; Turka,
                                                                                                                                                         GB/EMBL/DDBJ
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PID:g510901

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RESULT 13
I49056
bcl-x long -
                                      RESULT 14
S51761
SCL-X protein - rat
C;Species: Rattus morvegicus (Norway rat)
C;Species: Rattus morvegicus (Norway rat)
C;Date: 07-May-1995 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51761; S51762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:064373; EMBL:U10101; NID:g506647; PIDN:AAA82173.1; PID:g5066 R;Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M. submitted to the EMBL Data Library, November 1994 A;Description: II-5 inhibits anti-IgM-induced apoptosis in an immature B cell line throu A;Reference number: S52866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: I49055;
A; Accession: I49056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Immunol. 153, 4388-4398, 1994
A; Title: Cloning and molecular characterization of mouse
A; Reference number: I49055; MUID:95052604; PMID:7963517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
C;Accession: I49056; S52866
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
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submitted to the EMBL Data Library, November 1994 A;Reference number: S51761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-233 < KAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                              154 -RAWLQAQGGWDGFCHFF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 LQAQGGWDGFCHFF 170
                                                                                                                                                                                                                                                                                                                                   97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
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                                                                                                                                                                                                                 LEPWIQENGGWDTFVDLY 195
                                                                                                                                                                                                                                                                                              IVAFFSFGGALCVE-
                                                                                                                                                                                                                                                                                                                              VVTLVTFAGTLLERGPLVTARWKKWGFQPRLKEQEGDVARDCQRLVALLSSRL---MGQH 153
                                                                                                                                                                                                                                                                                                                                                                         PMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRD--GVNWGR
                                                                                                                                                                                                                                                                                                                                                                                                         PEAAV---LRSAAARLRQIHRSFFSAYLGY----PGNRFELVALMADSVLSDSPGPTWGR
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23.1%; Pred. No. 0.042;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 99.5; DB 2; Length 233; Pred. No. 0.042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                              -SVDKEMOVLVSRIASWMATYLNDH
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#status predict
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Gene 140, 291-292, 1994
A;Title: Cloning and sequencing of a cDNA encoding the A.Peference number: I53744; MUID:94193015; PMID:8144041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene bcl-2 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P49950; GB:L14680; NID:g408946; PIDN:AAA53662.1; PID:g408947
                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-236 < RES>
                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: I53744;
A; Accession: I53744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: I53744
R;Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
Gene 140, 291-992, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PID:g607178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-125, 189-233 < MI2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-233 < MIC>
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A;Status: prelimina
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                               FCHFFRTPF-PLAFWRKQLVQAFLSCLLTTAFIYL 199
                                                                                                                                          RDFAEMSSOLHLTPFTA----RGRF---ATVVEELFRD--GVNWGRIVAFFEFGGVMC- 155
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FVELYGPSMRPLFDFSWLSLKTLLSLALVGACITL
                                                                                                     RGPLVTARWKKWGFQPRLKEQEGDVARDCQRLV---ALLSSRLMGQH-RAWLQAQGGWDG 165
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; Pred. No. 0.04
17; Mismatches
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52;
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Search completed: June Job time : 40 secs

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Result
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-902-540-1114
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US-09-902-540-1866
US-09-902-540-1866
US-09-902-540-6388
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US-09-902-540-817
US-09-902-540-8186
US-09-902-540-8181
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US-09-252-991A-9680
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Sequence 13208, A
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838, App
879, App
889, App
896, App
2522, Ap
788, Ap
2238, Ap
238, Ap
2417, App
2817, Ap
48, Appl
31, Appl
9680, Ap
9641, Ap
9615, Ap
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5	44	43	C 42	41	40	39	38	37	c 36	35	34	C 33	c 32	μ	c 30	29	28
46.4	46.6	46.6	46.8	46.8	46.8	46.8	46.8	46.8	46.8	46.8	47	47	47.4	47.4	47.4	47.6	47.6
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US-09-252-991A-11619	US-10-327-189-3	US-09-949-016-1543	US-09-902-540-1261	US-09-902-540-1092	US-09-902-540-968	US-09-902-540-470	US-09-902-540-6509	US-09-902-540-9055	US-09-902-540-5345	US-09-902-540-9612	US-09-252-991A-14950	US-09-252-991A-14802	US-09-252-991A-10560	US-09-252-991A-10297	US-09-016-434-1256	US-09-902-540-749	US-09-902-540-7619
	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
11619, A	3, Appli	1543, Ap	.1261, Ap		968, App	470, App	6509, Ap	9055, Ap	5345, Ap	9612, Ap	14950, A	14802, A	10560, A	10297, A	1256, Ap	749, App	7619, Ap

ALIGNMENTS

ASSOCIATED
OF DETECTION AND USES THEREOF

RESULT 1 US-09-949-016-1466

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Sequence 1466, Application US/09949016
Patcent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSITITE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CL001307
CURRENT FPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1466
; LENGTH: 2508
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1466
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NUMBER OF SEQ ID NOS: 207012
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Local Similarity 46.2%;
les 257; Conservative
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314 AGCCCCGGCCCCACCTGGGGCAGAGTGGTGACGCTCGTGACCTTCGCAGGGACGCTGCTG 373
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                                                                                                                                           GTGCCCTGCGCGCCGCCTGCTCGTGGATGACTTCCGCACCCGAGGTTCGGGCCGCAAGC
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                                                                                            GETTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGTGCTCTCCGAC 313
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Pred. No. 0.00036;
D; Mismatches 294;
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US-09-949-016-13208
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Best Local S
Matches 257
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13208
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Patent No. 6812339
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CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(97989)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
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TYPE: DNA
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                                            GECTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGTGCTCTCCGAC
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                                                                            GTGCCCTGCGCGGCGGCCTGCTCGTGGATGACTTCCGCACCCGAGGTTCGGGCCGCAAGC
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                                                                                                                                                                                                      TGTCGGTGGACGAGGGGGGGGGGGGGGACATCCAGATGCTCCTGGAGGGCCGGGCCGGGG
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                CCCGGGAACCCCAAGCCGCGGAGCGGCGGACGGACTCACCCCCGTGTTCACG 89345
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US-09-902-540-794
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SEQ ID NO 794
SERGITH: 5808
TYPE: DNA
ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 162; Conserv
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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                                            GACCTTCGCAGGGACGCTGCTGGAGAGAGGGCCGCTGGTG
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ilarity 47.6%;
Conservative
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Pred. No. 0.00061;
0; Mismatches 178;
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APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sec.

FILE REFERENCE: 38-10 (1589) US/09/902,540

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 724
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US-09-902-540-8389
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TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences :
FILE REFERENCE: 38-10(15849)B
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/902,540
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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Pred. No. 0.00081;
0; Mismatches 237;
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; SEQ ID NO 879;
; LENGTH: 7186
; TYPE: DNA
; ORGANISM: Myxococcus x
; ORGANISM: Myxococcus x
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; TYPE: DNA
; ORGANISM: Myxococcus
US-09-902-540-8389
                                                                                                                                        Query Match 6.1%;
Best Local Similarity 46.5%;
Matches 175; Conservative
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Best Local Similarity
Matches 175; Conserv
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
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Pred. No. 0.0011;
D; Mismatches 201;
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Pred. No. 0.00061;
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US-09-902-540-8509
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SEQ ID NO 8509
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Best Local Similarity
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(11549)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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                                                                                                        AAGAAGTGGGGCTTCCAGCCGCGGCTAAAGGAGCAGGAGGGCGACGTCGCCCGGGACTGC
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Pred. No. 0.0015;
0; Mismatches 157;
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GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: MYXCOCOCCUS Xanthus Genome Service Control of the Steven C.
TITLE OF INVENTION: MYXCOCOCCUS Xanthus Genome Service CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 000/217,883
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
MUMBER OF SEQ ID NOS: 16825
                                                                                                         GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Serill Reference: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION WIMBER: US/09/902,540
PRIOR APPLICATION WIMBER: US/09/902,540
PRIOR APPLICATION WIMBER: 05/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID.NOS: 16825
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-2522
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US-09-902-540-2522
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LENGTH: 6482
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                                                                   SEQ ID NO 2522
LENGTH: 3198
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TYPE: DNA
ORGANISM: Myxococcus xanthus
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Pred. No. 0.0026;
0; Mismatches 157;
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GENERAL INFORMATION.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 1114

LENGTH: 17503

TYPE: DNA

ORGANISM: Myxococcus xanthus
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US-09-902-540-1114/c
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                                                                                                                       US-09-902-540-7886
                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-902-540-1114
                                                                   Sequence 7886, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION:
APPLICANT: Goldman, B
APPLICANT: Hinkle, G
APPLICANT: Slater, S
APPLICANT: Wiegand,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1114, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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 , Barry S.
, Gregory J.
, Steven C.
d, Roger C.
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Pred. No. 0.0059;
0; Mismatches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQ ID NO 7886
; LENGTH: 967
; TYPE: DNA
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849) B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 9238
                                                                         Query Match 5.7%;
Best Local Similarity 46.2%;
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9238, Application US/09902540 Patent No. 6833447
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Best Local Similarity 48.2%;
Matches 145; Conservative
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CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Myxococcus xanthus Genome
                                                                                                                                                                     TYPE: DNA ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                           LENGTH: 888
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                                     17 GCGAAGGCCCGGCCCCCAGCAGAGGCCGGACCATGGTTGACCAGTTGCGGGAGCGCACC 76
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GCGCTGAGGCTGCGCGTGGGGGGGATGGTCCGCCGGTGGTGGTGGTGGCGGAGCCGGAG 72
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                                                                         Score 50.2; DB 4;
Pred. No. 0.0056;
0; Mismatches 193;
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Pred. No. 0.0029;
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ACCATGGCCGACCCGCTGCGGGAGCGCACCGAGCTGTTGCTGGCCGACTACCTGGGGTAC 136

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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
ITILE OF INVENTION: Myxococcus xanthus Genome Seq FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2001-07-10
INUMBER OF SEQ ID NOS: 16825
SEQ ID NO 6388
LENGTH: 2199
TYPE: DNA
ORGANISM: Myxococcus xanthus
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                                                                                   GACCGCCCGGTGGAAGAAGTGGGGCTTCCAGCCGCGGCTAAAGGAGCAGGAGGGCGACGT
                                                                                                               GCTGTGGCCGCTGGTGGAGACCATGCGCTCGGCGCCACGCATCATGGCGGGCACGCCGGG
                                                                                                                                          GGGCAGAGTGGTGACGCTCGTGACCTTCGCAGGGACGCTGCTGGAGAGAGGGCCGCTGGT
                                                                                                                                                                    CTTCGAGCTGGTGGCGGATGGCGGATTCCGTCTCCGACAGCCCCGGCCCCACCTG
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44.68;
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Pred. No. 0.0079;
0; Mismatches 243;
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                                                                                   RESULT 15
US-09-902-540-987
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Patent No. 6833447;
GENERAL INFORMATION:
APPLICANT: Goldman,
APPLICANT: Hinkle,
APPLICANT: Slater,
                                                                   Sequence 987, Application
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
ITTLE OF INVENTION: Myxococcus xanthus Genom FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/99/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
INUMBER OF SEQ ID NOS: 16825
ISEO ID NO 424
LENGTH: 2585
TYPE: DNA
ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-902-540-424
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US-09-902-540-424
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GENERAL INFORMATION:
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Pred. No. 0.0083;
0; Mismatches 243;
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Barry S. Gregory J. Steven C.

US/09902540

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; APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 987
; LENGTH: 9818
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-987
Search completed: June 7, Job time : 285.584 secs
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                                                                                                    5477 TACAGCGCCACCGTGGGCGGTGGCCGCCGCGCGTGGCCGAACAGGGGGAGCGGCCCGA 5535
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                       2005, 18:17:14
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 2000000000
Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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21: /cgn2_6/ptodata/1/pubpna/US10R_PUBCOMB.seq:*

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24: /cgn2_6/ptodata/1/pubpna/US10R_PUBCOMB.seq:*

25: /cgn2_6/ptodata/1/pubpna/US10R_PUBCOMB.seq:*

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27: /cgn2_6/ptodata/1/pubpna/US10R_PUBCOMB.seq:*

26: /cgn2_6/ptodata/1/pubpna/US10R_PUB.seq:*

27: /cgn2_6/ptodata/1/pubpna/US10R_PUB.seq:*

28: /cgn2_6/ptodata/1/pubpna/US10R_PUB.seq:*

29: /cgn2_6/ptodata/1/pubpna/US10R_PUB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US10R_PUB.seq:*

21: /cgn2_6/ptodata/1/pubpna/US10R_PUB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

c 7 8	0 0 0 0 0 0 0	Result
320 320	887 506.8 457.2 457.2 324.6	
36.1 36.1	100.0 57.1 51.5 51.5 36.6	% Query Match Length DB ID
	548 548 548 548 874	Length I
20	204	8
US-10-363-345A-30993 US-10-363-345A-30994	16 US-10-071-174-1 9 US-09-912-599-3 9 US-09-764-847-311 14 US-10-092-154-311 20 US-10-363-345A-30995 20 US-10-363-345A-30996	SUMMARIES
Sequence 30993, A Sequence 30994, A	Sequence 1, Appli Sequence 3, Appli Sequence 311, App Sequence 311, App Sequence 3095, A Sequence 30996, A	Description

US-10-106-534-1 US-10-156-761-7129 US-10-156-761-7129 US-10-156-761-1284 US-10-156-761-15102 US-10-156-761-15-136891 US-10-425-114-28406 US-10-425-115-136891 US-10-425-115-131828 US-10-425-115-11828 US-10-425-114-23459 US-10-425-114-23459 US-10-425-114-24559 US-10-425-114-24559 US-10-425-114-27474 US-10-425-114-27479 US-10-425-1224-15026 US-10-425-134-15026 US-10-425-134-15026 US-10-425-134-15026 US-10-425-134-15026 US-10-437-963-4774 US-10-437-963-4774 US-10-203-295-3 US-10-203-295-3 US-10-203-295-3 US-10-479-435-34 US-10-479-435-34 US-10-479-435-34 US-10-479-435-34 US-10-479-435-34 US-10-479-435-34 US-10-479-435-37 US-10-479-435-37 US-10-479-435-34
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ALIGNMENTS

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                                                                                                                                                            LENGTH: 887
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-071-174-1
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US-10-071-174-1
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: KE, NING
APPLICANT: KE, NING
APPLICANT: KE, NING
APPLICANT: GODZIK, ADAM
TITLE OF INVENTION: APOPTOSIS MODULATOR BCL-B
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 087102-0272558
                                                                              Matches 887; Conservative
                                                                                                                                                                                                                                                 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10071174 Publication No. US20030176671A1
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/071,174
CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/267,166
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
                                                                                                 y Match 100.0%; Score 887; DB 16; Length 887; Local Similarity 100.0%; Pred. No. 3.4e-256;
                     1 CGGGCCAAGAAAACCAGCGAAGGCCCGGCCCCCAGCAGAAGGCCGGACCATGGTTGACCA 60
                                                                              0;
                                                                                Mismatches
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                                                                                Indels
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RESULT 2
US-09-912-599-3
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                                                                                          GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Bcl-2-like Polynucleotides, Polypeptides,
FILE REFERENCE: PT044P1
                                                                                                                                          Sequence 3, Application US/09912599 Patent No. US20020106731A1
CURRENT APPLICATION NUMBER: US/09/912,599
CURRENT FILLING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: PCT/US01/03080
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/179,487
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/180,697
PRIOR APPLICATION NUMBER: 60/180,697
PRIOR FILING DATE: 2000-02-07
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; SOFTWARE: PatentIn Ver. 2
; SEQ ID NO 3
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-912-599-3
                                                                                                     Sequence 311, Application US/09764847

Patent No. US20020132767A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC009

CURRENT APPLICATION NUMBER: US/09/764,847

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or
NUMBER OF SEQ ID NOS: 2003

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 311

LENGTH: 548
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US-09-764-847-311
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Best Local S
Matches 519
ORGANISM: Homo sapid
FEATURE:
NAME/KEY: SITE
LOCATION: (16)
OTHER INFORMATION: I
NAME/KEY: SITE
LOCATION: (20)
OTHER INFORMATION: I
                                                                                              TYPE: DNA
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Pred. No. 7.2e-142;
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antiboo FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 311
LENGTH: 548
TYPE: DNA
ODCHARTSM: Homo Saniens
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US-10-092-154-311
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                                                                                                                                                                                                                                                                           Sequence 311, A Publication No.
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Best Local Similarity 98.2%;
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NAME/KEY: SITE
LOCATION: (28)
OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (53)
NAME/KEY: misc feature
LOCATION: (16) OTHER INFORMATION: n equals a,t,g,
                                                     ORGANISM: Homo sapiens FEATURE:
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LOCATION: (26)
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o. US20030054375A1
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Pred. No. 6.2e-127;
2; Mismatches 5;
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US-10-363-345A-30995
; Sequence 30995, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 30995
; SEQ ID NO 30995
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LOCATION: (20)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
LOCATION: (26)
OTHER INFORMATION: n equals a,
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Pred. No. 6.2e-127;
2; Mismatches 5;
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ORGANISM: Artificial Sequence

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; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-363-345A-30995
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                                                                                                                                                     APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: E01/127
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 30996
LENGTH: 874
                                                                                                                                                                                                                                                                                                               Sequence 30996, Application US/10363345A Publication No. US20040234960A1 GENERAL INFORMATION:
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Best Local Similarity
              Matches
                                          Query Match
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                                                                   OTHER INFORMATION:
OTHER INFORMATION:
-10-363-345A-30996
                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
              Local Similarity
nes 405; Conserv
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CpG-island
                                                                                  chemically treated genomic DNA CpG-island No: 30996
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75.1%;
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             Score 324.6; DB 20; Pred. No. 5.9e-87; 0; Mismatches 134;
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Pred. No. 5.9e-87;
0; Mismatches 134;
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US-10-363-345A-30993/c
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: extosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: B01/1227
                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 30993
LENGTH: 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30993, Application US/10363345A Publication No. US20040234960A1
                                                                                                                                                                                     Matches 401;
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                             chemically treated genomic CpG-island No: 30993
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Pred. No. 1.4e-85;
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3
TITLE REFERENCE: E01/1227
TITLE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 30994
LENGTH: 874
TYPE-.NB 74
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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CTCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTC
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74.8%;
                                                                                                                                                                                                                                                                                                                                                                             Score 320; DB 20;
Pred. No. 1.4e-85;
0; Mismatches 135;
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        TITLE OF INVENTION: A Method To Assess Quorn TITLE OF INVENTION: A Method To Assess Quorn TITLE OF INVENTION: Communities
FILE REFERENCE: HER-0056
CURRENT APPLICATION NUMBER: US/10/338,110
CURRENT FILING DATE: 2003-01-07
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin version 3.2
SEQ ID NO 119
LENGTH: 536
TYPE: DNA
ORCANTON
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US-10-338-110-119

; Sequence 119, Application US/10338110

; Publication No. US20040023254A1

; GENERAL INFORMATION:
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US-09-908-975-15549
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APPLICANT: WASSERMAN, A
APPLICANT: MINTZ, Elia
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 15549
LENGTH: 60
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Best Local Similarity
                                                                                                                                                                                                                    APPLICANT: Fuhrmann, Jeffry APPLICANT: Romesser, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-07-28 NUMBER OF SEQ ID NOS: 32337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 36688-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        565 CCCCTTTCCACTGGCTTTTTTGGAGAAAACAGCTGGTCCAGGCTTTTTCTGTCATGCTTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%; Score 60; DB 10; larity 100.0%; Pred. No. 8.9e-08; Conservative 0; Mismatches 0;
                                                                                                                                                                                                   Quorum
                                                                                                                                                                                                 Sensing
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                                                                                                                                      NAME/KEY: misc_feature; LOCATION: (517)...(517); OTHER INFORMATION: n is a, US-10-338-110-119
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Best Local Similarity
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LOCATION: (226)...(226)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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LOCATION: (357)..(357)
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LOCATION: (213)..(213)
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LOCATION: (87)..(87)
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LOCATION: (21)..(21)
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OTHER INFORMATION: n is
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LOCATION: (273)..(273)
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LOCATION: (419)..(419)
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                                                       118 GGCCGACTACCTGGGGTACTGCGCCCGGGAACCCGGCACCCCGAGCCGGCGCCATCCAC
  GCCCGAGGCCGCCGTGCTGCGCTCCGCCGGCCGAGGTTACGGCAGATTCACCGGTCCTT
                               SSKCTACVTSBTSGCSHKVRGMVSVYVGBDHATSKKYGGHTGYGCSCGSCTGHTDCCBAC
                                                                                  6.3%;
llarity 15.2%;
Conservative 194
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Pred. No. 3.3e-06;
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US-10-437-963-2495
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LENGTH: 989
                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                               Local Similarity
es 156; Conserv
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308 TCCGACAGCCCCGGCCCCACCTGGGGCAGAGTGGTGACGCTGGTGACCTTCGCAGGGACG 367
                                                                                                                                                                                                                                     68 GAGCGCACCATGGCCGACCCGCTGCGGGAGCGCACCGAGCTGTTGCTGGCCGACTAC 127
                                                                                                                         GCCGTGCTGCGCCGCCGGCCCAGGTTACGGCAGATTCACCGGTCCTTTTTCTCCGCC
                                             CACTCGGCGGACCACGCGGGCGTGGAGGGGCAGTACCACCTGCTGCTGCAGGGCGTCGTG
                                                                                                                                                                                                           GACGGCACCGTGCCGACCACCTCCACAACTTCGAGCACGCGTCCATCTCCCTCGCG 338
                                                                     TACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGTGCTC
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Cao, Yor
Wu, Wei
                                                                                                 GCCGTGTCGCAGCTCGTCGCCGCCGCTGGCGTTCGCGCAGCAGCTGATGCTGTTCCACCTC
                                                                                                                                                       CTGCTCGTCTACGCCGCCGCCGCCGCCGCCCTCGACGTGGCCCGGGTGCCGCACGGCCGC
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Score 55.2; DB 19; Pred. No. 7.3e-06; 0; Mismatches 168;

Length Indels

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Gaps

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Sequence 2495, Application US/10437963
Publication No. US20040123343A1
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT FILION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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                                                                                                                                                                                                                                                             Barbazuk, Brad
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RESULT 13
US-10-106-534-1
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                                                                            Sequence 1, Application US/10106534
Publication No. US20020168668A1
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                                                           GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OP INVENTION: 14691, A Human Glutamate Receptor Family
TITLE OP INVENTION: Member and Uses Therefor
FILE REFERENCE: MPIOI-042P1RM
CURRENT FAPLICATION NUMBER: US/10/106,534
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: 60/279,086
PRIOR FILING DATE: 2001-03-27
NUMBER: FILING DATE: 2001-03-27
APPLICANT: Curtis, Rory A.J.
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: 14691, A Human Glutamate
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TYPE: DNA
ORGANISM: homo &
FEATURE:
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SOFTWARE: FastSEQ for Windows Version
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LOCATION: (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 AACCTGAGCTTGGAGCTGGTGGTCGCCGCGCCCCCCGCCGACCCCGCCTCGCTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 193;
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   Receptor Family
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; TYPE: DNA
; ORGANISM: homo :
; FEATURE:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...
US-10-106-534-1
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US-10-425-115-143369
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                                                                                                                                                                                                                                                                    Sequence 143369, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                          NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 143369
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Best Local Similarity
Matches 185; Conserv
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OTHER INFORMATION: Clone ID: MRT4577_6222C.1
-10-425-115-143369
                                                                                                                       APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT PIPLICATION UNMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                    APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/106,534
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: 60/279,086
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Member and Uses Therefor FILE REFERENCE: MPI01-042PIRM
                              TYPE: DNA
ORGANISM: Zea mays
FEATURE:
                                                                              LENGTH: 1743
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nilarity 48.4%;
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Pred. No. 1.1e-05;
0; Mismatches 193;
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US-10-156-761-7129
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                                                    Query Match
Best Local S
Matches 165
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                     SEQ ID NO 7129
LENGTH: 954
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Best Local Similarity
Matches 226; Conserv
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                    TYPE: DNA
ORGANIAM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(954)
-10-156-761-7129
                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                APPLICANT: SAKAKÍ, YOSHİYUKI
APPLICANT: HATTORİ, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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al Similarity 47.0%;
165; Conservative
23 GCCCGGCCCCCAGCAGAGGCCGGACCATGGTTGACCAGTTGCCGGGAGCGCACCATG
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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Pred. No. 1.2e-05;
                                                   Score 53.4; DB 15;
Pred. No. 2.5e-05;
0; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 232;
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Search completed: June 7, 2005, 18:04:16
Job time: 839.797 secs

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Result
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6.6	6.6	6.7	6.7	6.8	6.8	6.8	6.9	7.1	7.2	7.8	9.5	10.9	11.0	11.2	12.0	12.1	12.1	12.9	13.0	13.2
706	931	1070	935	606	1552	1267	661	330	925	925	313	339	615	363	399	352	440	130	380	638
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AJ455155	CK412737	BZ557810	CNS006XK	BP111813	AG430101	CL476590	CE629081	CA556079	CNS0091P	CNS0091P	AI467076	AI604990	BM230283	BG084666	AA623872	AA426934	BY029830	AA098865	BY029358	BM228756
AJ455155 AJ455155	CK412737 AUF_IpGil	BZ557810 pacs1-60_	AL066051 Drosophil	BP111813 BP111813	AG430101 Mus muscu	CL476590 SAIL_258_	CE629081 tigr-gss-	CA556079 K0206H12-	AL053013 Drosophil	AL053013 Drosophil	AI467076 vd09e08.x	AI604990 vf22b11.x	BM230283 K0293B04-	BG084666 H3103E12-	AA623872 vq73g11.s	AA426934 vf22b11.s	BY029830 BY029830	AA098865 zk84f02.s	BY029358 BY029358	BM228756 K0267E03-

ALIGNMENTS

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CA777633/c
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                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 617-495-1812

Pax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information

Washington University Genome Sequencing Center For information
                                                                                                                                                                                                                                                                                             obtaining a clone please contact: Dr. (hinoue@im.wustl.edu)
Possible reversed clone: similarity on Seq primer: -40RP from Gibco
High quality sequence stop: 392.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hirosh Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity & MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 715)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce, M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D. Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Scardenas,M., Gibbons,M., McCamn,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA777633 715 bp mRNA linear EST 03-DEC-2002 ip19a09.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6217625 5' similar to TR:Q9Z0F3 Q9Z0F3 BCL-2 HOMOLOG: ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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/organism="Homo sapiens"

/mol type="mRNA"

/mol type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6217625"

/tissue_type="Purified pancreatic islet".

/lab_host="DH10B"

/clone_lib="HR85 islet"

/clone_lib="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-);

NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
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Best Local :
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                                                             National Institute on Aging/National Institutes of Health 33 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community.
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
plate: H3058 row: C column: 03
Seq_primer: -21M13 Reverse
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H3058C03-5', mRNA sequence.
                                                                                                                                                                                                                                   Contact: George J. Kargul Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 626)

Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, F. Wood, W.H. III, Becker, K.G. and Ko, M.S.H.

Genome wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG080862
BG080862.2 GI:40014930
EST.
                                                                                                                                                                                                                                                                                  On Jan 26, 2001 this sequence version replaced gi:12563419 Other_ESTs: H3058C03-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus (house mouse)
                                            quality sequence stop:
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XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
Location/Qualifiers
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ches 21;
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                                                                                                                                               CAGCACCGCGCCTGGCTGCAGGCTCAGGGCGGCTGGGATGGCTTTTGTCACTTCTTCAGG
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                                                      ACCCCTTTCCACTGGCTTTTTGGAGAAAACAGCTGGTCCAGGCTTTTCTGTCATGCTTG
                                                                                                                                                                                                                  ATAGTGACCCGAGACTGCTGTCTCATAGTGAACTTTCTGTATAATCTGCTCATGGGGCGT
                                                                                                                                                                                                                                                            GACGTCGCCCGGGACTGCCAGCGCCTGGTGGCCTTGCTGAGCTCGCGGCTCATGGGG----
                                                                                                                                                                                                                                                                                                              TACATGGCTGTCAAGCAGAAGA--
                                                                                                                                                                                                                                                                                                                                                          CTGGTGACCGCCCGGTGGAAGAAGTGGGGCTTCCAGCCGCGCTAAAGGAGCAGGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                         AGCTGGAGCCAACTGGTGATGCTCCTGGCCTTCGCGGGGACGCTTATGAATCAAGGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGTGCTCTCCGACAGCCCCGGCCCC 325
                        AATCCTTTACCGCTCGGCTTCTGGAGAAGATTGCTGATTCAGGCTTTTCTGTCAGGCTTC
                                                                                                                    CGGCACCGCCCAGGCTGGAGGCTCTCGGCGGCTGGGATGGCTTTTTGCCGCTTCTTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NIA Mouse 15K cDNA Clone Set"
//clone_lib="NIA Mouse 15K cDNA Clone Set"
//clone="Vector: pSPORT1; Site 1: Sall; Site 2: Not1; This
clone is among a rearrayed set of 15,247 clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5
embryos, and E12.5 female mesonephros/gonad) and one
newborn ovary cDNA library. Average insert size 1.5 kb.
All source libraries are cloned unidirectionally with
Oligo(dT)-Not primers. References include: (1)
Genome-wide expression profiling of mid-gestation
placenta and embryo using a 15,000 mouse developmental
cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97:
9127-9132; (2) Large-scale cDNA analysis reveals phased
gene expression patterns during preimplantation mouse
development, 2000, Development, 127: 1737-1743; (3)
Genome-wide mapping of unselected transcripts from
extraembryonic tissue of 7.5-day mouse embryos reveals
enrichment in the t-complex and under-representation on
the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
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/mol_type="mRNA"
/strain="C57BL/6J"
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/dev_stage="Clones arrayed from a variety of cDNA
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/db_xref="taxon:10090"
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Pred. No. 2.4e-47;
0; Mismatches 193;
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Indels Length

25;

Gaps

77

GGGATCTGGGGAATCGTGTC

359

445

317 385 257

197

137

479

562 419

539 622

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AUTHORS
TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Dr. Kathleen Horner, Stanford University CDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     875 bp mRNA linear ES: AGENCOURT 30259012 NIH MGC 256 Mus musculus cDNA clone IMAGE:30935405 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 659.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 875)
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CO798715.1 GI:50986895
                                                                                                                  GAACCCGGCACCCCGAGCCGGCGCCCATCCACGCCGAGGCCGCGCGTGCTGCGCTCCGCG
                                                                                                                                                                                              GACCCGCTGCGGGAGCGCACCGAGCTGTTGCTGGCCGACTACCTGGGGTACTGCGCCCGG
                                                   GCCGCCAGGTTACGGCAGATTCACCGGTCCTTTTTCTCCGCCTACCTCGGCTACCCCGGG 265
                                                                                                                                                           GACCCACTGCATGAACGCACTAGACGGCTGCTGTCTGACTACATATTCTTCTGCGCACGG
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/clone_lib="NIH MGC 256"
/clone_lib="NIH MGC 256"
/note="Organ: ocyte; Vector: pExpress-1; Site_1: EcoRV;
/note="Organ: ocyte; Vector: pExpress-1 Site_other:
5'-pGACTAGTTCTAGATCGCGAGCGGCCCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb resulted in an average insert size of 1.2 kb. This is a primarylibrary (normalized primary library is NIH MGC 257)
and was constructed by Express Genomics (Frederick, MD).
                                                                                                                                                                                                                                                                                                                       and was constructed by Express Genomics Note: this is a NIH_MGC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol type="mRNA"
/db xref="taxon:10090"
/clone="IMAGE:30935405"
/lab_host="DH10B TonA"
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Pred. No. 4.1e-47;
0; Mismatches 206;
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CF915355
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                                                                                                                                                                                                                                                                                Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0978 row: E column: 08
                                                                                                                                                                                                                                                                                                                                       Contact: Dawood
                                                                                                                                                                                                                                                                                                                                                            11544199
                                                                                                                                                                                                                                                                                                                                                                              21429098
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                primer: M13 Reverse
                                                   /db_xref="niaEST:B0978E08-5"
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/strain="C57BL/6J"
                                                                                                                                                                            Location/Qualifiers
                    'dev_stage="Unfertilized Egg"
'lab_host="DH10B"
clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:38186557
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Sciurognathi; Muridae,
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ACCTGGGGCAGAGTGGTGACGCTCGTGACCTTCGCAGGGACGCTGCTGGAGAGAGGGCCG 385
                                       CGCTTCTACCTGCCCAACTGTGACCAACTAAATGACAGATGTGTG
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CGATCTTACCTACCTGCTGTGAACCCTCTAAGGAACATTCTGGG
                                                                                                               TTTGCAACAGCCATCTTTTTATCTGGAAACGTTTAT----AAGTTTAAAATTTTTAAAG
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CF915355

B0978E08-5 NIA Mouse Unfertilized Egg cDNA Library
musculus cDNA clone NIA:B0978E08 IMAGE:30479767 5', EST 05-NOV-2003 (Long 1) Mus mRNA sequence.

PCR amplification

Euteleostomi;
; Murinae; Mus

Mus.

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Query Match
Best Local Similarity
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596
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                             CGCTTCTACCTGCCCAACTGTGACCAACTAAATGACAGAT
                                                                                                                                                                                                                                          ACCCCCTTTCCACTGGCTTTTTTGGAGAAAACAGCTGGTCCAGGCTTTTTCTGTCATGCTTG
                                                                                                                                                                                                                                                                                                           CGGCACCGCCCAGGCTGGAGGCTCTCGGCGGCTGGGATGGCTTTTTGCCGCTTCTTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACGICGCCCGGGACTGCCAGCGCCTGGTGGCCTTGCTGAGCTCGCGGCTCATGGGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGTGACCGCCCGGTGGAAGAAGTGGGGCTTCCAGCCGCGCTAAAGGAGCAGGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCTGGGGCAGAGTGGTGACGCTCGTGACCTTCGCAGGGACGCTGCTGGAGAGAGGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATCGCCTGGAGCTGGTGAAACAGATGGCAGATAAGTTGCTCTCCAAAGACCAAGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGTGCTCTCCGACAGCCCCGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTAGGCAGATCCAGCAGGAGCACCAAGAATTTTTTTCCTCCTTCTGCGAAAGCCGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCGCCAGGTTACGGCAGATTCACCGGTCCTTTTTCTCCGCCTACCTCGGCTACCCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACCCACTGCATGAACGCACTAGACGGCTGCTGTCTGACTACATATTCTTCTGCGCACGG
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                                                                                                     TTTGCAACAGCCATCTTTTTTATCTGGAAACGTTTAT----AAGTTTAAAATTTTTAAAG
                                                                                                                                             TTAACAACAGCCTTCATTTATCTCTGGACACGATTATTATGAGTTTTTAAAACTTTTTAACC
                                                                                                                                                                                                        AATCCTTTACCGCTCGGCTTCTGGAGAAGATTGCTGATTCAGGCTTTTCTGTCAGGCTTC
                                                                                                                                                                                                                                                                                                                                                     CAGCACCGCGCCTGGCTGCAGGCTCAGGGCGGCTGGGATGGCTTTTGTCACTTCTTCAGG
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CGATCTTACCTACCTACCTGTGAACCCTCTAAGGAACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B B. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sall; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetice, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.5%;
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Pred. No. 4.3e-47;
0; Mismatches 203
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CO814648
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ORGANISM
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Best Local S
Matches 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                       412;
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                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: NDAM1195 row: i column: 19 High quality sequence start: 5 High quality sequence stop: 666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institutes of Health, Mammalian Gene Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CO814648
AGENCOURT 30246837 NIH MGC 256 Mus IMAGE: 30937746 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                      GCCGCCAGGTTACGGCAGATTCACCGGTCCTTTTTCTCCGCCTACCCTCGGCTACCCCGGG
                                                                                                                                                                                                                                                                                    GAACCCGGCACCCCGAGCCGGCGCATCCACCCCGAGGCCGCCGCGCTGCTGCTCCGCG
ACCTGGGGCAGAGTGGTGACGCTCGTGACCTTCGCAGGGACGCTGCTGGAGAGAGGGCCG
                                                                                                                                                                                                                                                   GAGCCGGACACCCCAGAGCCACCGCCCACGTCTGTCGAGGCGGCCTTGCTTCGCTCTGTG
                                                                                                                                                                                                                                                                                                                                            GACCCACTGCATGAACGCACTAGACGCTGCTGTCTGACTACATATTCTTCTGCGCACGG
                                                                                                                                                                                                                                                                                                                                                                                      GACCCGCTGCGGAGCGCACCGAGCTGTTGCTGGCCGACTACCTGGGGTACTGCGCCCGG
                                                                                                                AACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCCGTGCTCTCCGACAGCCCCGGCCCC
                                                                          AATCGCCTGGAGCTGGTGAAACAGATGGCAGATAAGTTGCTCTCCAAAGACCAAGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B TonA"
/clone lib="NIH MGC 256"
/clone lib="NIH MGC 256"
/clone lib="NIH MGC 256"
/note="Organ: occyte; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; cDNA was primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
the EcoRV/Not1 sites of pExpress-1. Size-selection >0.5 kb
resulted in an average insert size of 1.2 kb. This is a
primarylibrary (normalized primary library is NIH MGC 257)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="IMAGE:30937746"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 233.4; DB 7
Pred. No. 1.2e-46;
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RESULT 6
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                  JOURNAL
MEDLINE
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                                                                                                                                                        Nikaido, I., Osato, N., Saito, R., Suuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forreet, A., Frazer, K.S., Gasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Wallana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomite, M.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Walley, L., Yuan, Z., Zavolan, M., Shinaka, K., Kawai, K., Kawai, K.,
Sakazume, M., Sato, K., Shiraki, T., Waki, K., Kawai, X., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Yashizume, W., Imotani, K., Ishii, Y.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Roders, J., Biria, A., and Havashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA linear EST 17-DEC-BY735639 RIKEN full-length enriched, 1 cell embryo Mus musculus cDNA clone IOC0031F16 5', mRNA sequence.

BY735639
                                                                                            Rogers, J., Birney, E. and Hayashizaki, Y. Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY735639.1 GI:27148766
                                                                    Nature 420,
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Best Local Similarity Matches 463; Conserv
                                                                         386 CTGGTGACCGCCCGGTGGAAGAAGTGGGGCTTCCAGCCGCGCTAAAGGAGCAGGAGGGC 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
  Please visit our web site (http://genome.gsc.riken.go.jp) for
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TACATGGCTGTCAAGCAGAAGA
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/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="10C0031F16"
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dev_stage="1 cell embryo"
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Pred. No. 3.4e-46;
0; Mismatches 242
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       GGGATCTGGGGGAATCGTGTC
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RESULT 7
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588 bp mRNA linear EST 19-NOV-200 K0229B10-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus musculus cDNA clone NIA:K0229B10 IMAGE:30047445 5', mRNA sequence. CA557550
                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0229 row: B column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 588)
Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C.A., Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_ESTs: K0229B10-3
Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                         primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                       quality sequence stop:
    /note="Vector: pSPORT1 (Invitrogen); Site_1: Sall; Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
                                                                                                                        /clone="NIA:K0229B10 IMAGE:30047445"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
                                                                                            /clone_lib="NIA Mouse Unfertilized Egg cDNA Library
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                /db_xref="niaEST:K0229B10-5N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                      /strain="C57BL/6J"
                                                                                                                                                                                                                                        mol_type="mRNA"
                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                         588
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758 bp
AGENCOURT 30246635 NIH MGC 256 Mus
IMAGE:30937853 5', mRNA sequence.
C0799635
C0799635.1 GI:50987815
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a long-transcript enriched cDNA library (Ref. Genome Res
11: 1553-1558 (2001). [PMID: 11549]). Total RNAs were
extracted from a pool of 1488 unferrillized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
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Length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 GACCCGCTGCGGGAGCGCACCCGAGCTGCTGGCCGACTACCTGGGGTACTGCGCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                           ACCCCCTTTCCACTGGCTTTTTGGAGAAAAACAGCTGGTCCAGGCTTTTCTGTCATGCTTG
                                                                                                                                                                                                                                                                                      GACGTCGCCCGGGACTGCCAGCGCCTGGTGGCCTTGCTGAGCTCGCGGCTCATGGGG---
                                                                                                                                                                                                                                                                                                                                                                          CTGGTGACCGCCGGTGGAAGAAGTGGGGCTTCCAGCCGCGGCTAAAGGAGCAGGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCTGGGGCAGAGTGGTGACGCTGCGTGACCTTCGCAGGGACGCTGCTGGAGAGAGGGCCG
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TTTGCAACAGCCATCTTTTTTATCTGGAAACGTTTATAA
                            TTAACAACAGCCTTCATTTATCTCTGGACACGATTATTA
                                                                                    AATCCTTTACCGCTCGGCTTCTGGAGAAGATTGCTGATTCAGGCTTTTCTGTCAGGCTTC
                                                                                                                                                                 CGGCACCGCGCCAGGCTGGAGGCTCTCGGCGGCTGGGATGGCTTTTGCCGCTTCTTCAAG
                                                                                                                                                                                                          CAGCACCGCCCCGGCTGCAGGCTCAGGGCGGCTGGGATGGCTTTTGTCACTTCTTCAGG
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                                                                                                                                                                                                                                                                                                                               TACATGGCTGTCAAGCAGAAGA-------
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Pred. No. 2.2e-44;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NDAM1195 row: n column: 06
High quality sequence stop: 623.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Kathleen Horner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, N
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
ATAGTGACCCGAGACTGCTCTCATAGTGAACTTTCTGTATAATCTGCTCATGGGGCGT
                                     GACGTCGCCGGGACTGCCAGCGCCTGGTGGCCTTGCTGAGCTCGCGGCTCATGGGG--- 502
                                                                                                             CTGGTGACCGCCCGGTGGAAGAAGTGGGGCTTCCAGCCGGGCTAAAGGAGGAGGAGGGC 445
                                                                                                                                                                                             AATCGCCTGGAGCTGGAAACAGATGGCAGATAAGTTGCTCCCAAAGACCAAGACTTC
                                                                                                                                                                                                                                                                                         AACCGCTTCGAGCTGGTGGCGCTGATGGCGGGATTCCGTGCTCTCCGACAGCCCCGGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: OCCyte; Vector: pExpress-1; Site_1: ECORV; Site_2: Not1; CDNA was primed using oligo-dT primer: 5'-pGACTAGTTCTAGATCGCGAGCGGCCCC(T)25-3' and cloned into the ECORV/NotI sites of pExpress-1. Size-selection >0.5 kb resulted in an average insert size of 1.2 kb. This is a primarylibrary (normalized primary library is NIH MGC 257) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH MGC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B TonA"
/clone_lib="NIH_MGC_256"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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64.6%;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 220.8; DB 7; Length 758; Pred. No. 1.6e-43; 0; Mismatches 182; Indels 21
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Sciurognathi; Muridae; Murinae; Mus
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: NDAM1198 row: d column: 06
High quality sequence start: 19
High quality sequence stop: 527.
Location/Qualifiers
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Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 821)
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AGENCOURT 30256704 NIH MGC 256 Mus IMAGE: 30938765 5', mRNA sequence.
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                                       ccceeeaaaccceecacccceaeccececcacccacecceaeeccecereccereccere
                                                                                                                                TGGCCGACCCGCTGCGGGAGCGCACCGAGCTGTTGCTGGCCGACTACCTGGGGTACTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCCCCTTTCCACTGGCTTTTTGGAGAAAAACAGCTGGTCCAGGCTTTTTCTGTCATGCTTG 622
CACGGGAGCCGGACACCCCAGAGCCACCGCCCACGTCTGTCGAGGCGGCCTTGCTTCGCT
                                                                                      TGGCTAAGACAGTTTCGGCCGGAATCCCGGGATTGCTGTCTGACTACATATTCTTCTGCG
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                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                   the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb resulted in an average insert size of 1.2 kb. This is a primarylibrary (normalized primary library is NIH MGC 257) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library"
                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: oocyte; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; cDNA was primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:30938765"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
mol_type="mRNA"
db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus
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61.3%;
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Pred. No. 9.7e-42;
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JOURNAL COMMENT
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                                                                                                                                                                                                 Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, U
                                                                                                                                                                                                                                                                                                                            Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDN
                                                                                                                                                                        Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0274 row: C column: 06
                                                                                                                                                                                                                                                              Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                             Unpublished (2001)
Other_ESTs: K0274C06-3
                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
1 (bases 1 to 524)
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                      primer: M13 Reverse
                                                                                                                                     quality sequence stop:
                              /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                     Location/Qualifiers
              db_xref="niaEST:K0274C06-5N"
                                                                  organism="Mus musculus"
_xref="taxon:10090"
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Best Local Similarity
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                                ရှ:
                                                                                        CAGCTGGTCCAGGCTTTTCTGTCATGCTTGTTAACCAGCCGTCCATTTATCTCTGGACA
                                                                                                                                                           GGCTGGGATGGCTTTTGTCACTTCTTCAGGACCCCCTTTCCACTGGCTTTTTTGGAGAAAA
                                                                                                                                                                                                            AACTITICIGTATAATCTGCTCATGGGGCGTCGGCACCGCGCCAGGCTGGAGGCTCTCGGC
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CG 524
                                                                    TTGCTGATTCAGGCTTTTCTGTCAGGCTTCTTTTGCAACAGCCATCTTTTTTATCTGGAAA
                                                                                                                                       GGCTGGGATGGCTTTTGCCGCTTCTTCAAGAATCCTTTACCGCTCGGCTTCTGGAGAAGA
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                                  654
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treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs.

Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="NIA:K0274C06 IMAGE:30051773"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="NIA Mouse Unfertilized Egg cDNA Library (Long)"
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116 CTGGCCGACTACCTGGGGTACTGCGCCCGGGAACCCCGGGCACCCCGGGCCCATCC 175 176 ACGCCCGAGGCCGCGCGCGCGCCCGCCGCCCAGGTTACGGCAGATTCACCGGTCC TCTGTCGAGGCGGCCTTGCTTCGCTCTGTGACTAGGCAGATCCAGCAGGAGCACCAAGAA CTGTCTGACTACATATTCTTCTGCGCGCGCGGGAGCCCGGACACCCCAGAGCCACCGCCCACG 23.3%; 0, Score 206.4; DB 6 Pred. No. 5.3e-40; Mismatches 171; 6; Indels Length 21; Gaps 235 60

180

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342

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652 462

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JOURNAL COMMENT
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238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 763)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: NDAM1198 row: 1 column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                               CTCCGCCTACCTCGGCTACCCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTC
                                                                                                                                                                                                                                                                                                                                                                             CGAGGCCGCCGTGCCGCCCGCCGGCCAGGTTACGGCAGATTCACCGGTCCTTTTT
                                                                                                                                                                                                                                                                                                                                      CGAGGCGGCCTTGCTTCGCTCTGTGACTAGGCAGCAGCAGGAGCACCAAGAATTTTT
                                                                                                                        AGGGACGCTGCTGGAGAGAGGGCCCGCTGGTGACCGCCCGGTGGAAGAAGTGGGGCTTCCA
                                                                                                                                                                  GTTGCTCTCCAAAGACCAAGACTTCAGCTGGAGCCAACTGGTGATGCTCCTGGCCTTCGC
                                                                                                                                                                                                                                                     TTCCTCCTTCTGCGAAAGCCGGGGCAATCGCCTGGAGCTGGTGAAACAGATGGCAGATAA
                                       GCCGCGGCTAAAGGAGCAGGAGGGCGACGTCGCCCGGGACTGCCAGCGCCTGGTGGCCTT
                                                                                 GGGGACGCTTATGAATCAAGGCCCTTACATGGCTGTCAAGCAGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=Torgan: oocyte; Vector: pExpress-1; Site_1: EcoRV; Site 2: NotI; cDNA was primed using oligo-dT primer: 5'-pGACTAGTTCTAGATCGCAGCGGCGCCCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb resulted in an average insert size of 1.2 kb. This is a primarylibrary (normalized primary library is NIH MGC 257) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH MGC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="mRNA"
/db xref="taxon:10090"
/clone="IMAGE:30938958"
/lab_host="DH10B TonA"
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Pred. No. 2.6e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasoe, S., Dietrich, N., DuBuque, T., Ravello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardia, B., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J. Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA005293 206 bp mRNA linear zh93a11.r1 Soares fetal_liver_spleen_INFLS_S1 Homo clone IMAGE:428828 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 849 Std Error: 0.00
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97044478
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                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: mob.REGA+ET
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/dev_stage="20 week-post conception fetus"
/lab host="DH10B (ampicillin resistant)"
/clone lib="Soares fetal liver spleen INFLS S1"
/note="Torgan: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
This is a subtracted verson of the original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5'
                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="GDB:1328597"
/db_xref="taxon:9606"
                                                                                                                                                                                                        clone="IMAGE: 428828"
                                                                                                                                                                                          sex="male"
                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA561864 478 bp mRNA linear EST 19-NOV-200 K0293B04-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus musculus cDNA clone NIA:K0293B04 IMAGE:30053583 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_ESTs: K0293B04-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; En
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; I
1 (bases 1 to 478)
Piao;Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A.,
Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNI
                                                                                                                                                                                                                                                                                                                                                                       National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnaelgsun.grc.nia.nih.gov Plate: K0293 row: B column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pSPORT1 (Invitrogen); Site_1: Sall; Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="mRNA"
                                                                                      /clone_lib="NIA Mouse Unfertilized Egg cDNA Library
                                                                                                                     /tissue_type="Unfertilized Egg"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                              (Long)
                                                                                                                                                         clone="NIA:K0293B04 IMAGE:30053583"
                                                                                                                                                                             db_xref="taxon:10090"
                                                                                                                                                                                           db_xref="niaEST:K0293B04-5N"
                                                                                                                                                                                                                   strain="C57BL/6J"
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Pred. No. 1.3e
0; Mismatches
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ACCESSION VERSION

CO811958 CO811958.1 GI:51030584

SOURCE

ORGANISM

Mus musculus (house Mus musculus

Eukaryota;

Metazoa;

Chordata; mouse)

Craniata;

Vertebrata;

Euteleostomi;

KEYWORDS

RESULT 14 CO811958

DEFINITION

CO811958 893 bp AGENCOURT 30259915 NIH MGC 256 M IMAGE:30939397 5', mRNA sequence

Mus

clone

06-AUG-2004

mRNA musculus

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 AATCCTTTACC
                            ACCCCCTTTCC 573
                                                                                   CAGCACCGCGCCTGGCTGCAGGCTCAGGCCGGCTGGGATGGCTTTTGTCACCTTCTTCAGG
                                                                                                                  ATAGTGACCCGAGACTGCTGTCTCATAGTGAACTTTCTGTATAATCTGCTCATGGGGCGT
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                                                       CGGCACCGCCAGGCTGGAGGCTCTCGGCGGCTGGGATGGCTTTTTGCCGCTTCTTCAAG
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62.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: NDAM1199 row: n column: 14 High quality sequence stop: 538.
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Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Kathleen Horner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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                                CAGCACCGCGCCTGGCTGCAGGCTCAGGGCGCTGGGATGGCTTTTGTCACTTCTTCAGG 562
                                                                                                                                             GACGTCGCCCGGGACTGCCAGCGCCTGGTGGCCCTTGCTGAGCTCGCGGCTCATGGGG---
                                                                                                                                                                                                               TACATGGCTGTCAAGCAGAAGA--------GGGATCTGGGGAATCGTGTC
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                                                                                                                                                                                                                                                                   CTGGTGACCGCCCGGTGGAAGAAGTGGGGGCTTCCAGCCGCGGCTAAAGGAGCAGGAGGGC
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//clone lib="NIH_MGC_256"
//clone lib="NIH_MGC_257"
//clone lib="NIH_MGC_
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/db_xref="taxon:10090"
/clone="IMAGE:30939397"
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Pred. No. 6.4e-31;
0; Mismatches 177
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This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further inform M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT.
Location/Qualifiers
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Tel: +49 30 32639 101
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates;
1 (bases 1 to 535)
Ebert, L., Heil, O., Hennig, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      535 bp mRNA linear EST 10-FEB-2003 BX119239 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGp998N01170 ; IMAGE:40052, mRNA sequence.
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bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
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RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
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Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2003)
Contact: Ina Rolfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Radelof, U., Schneider, D.
Human UnigeneSet - RZPD3
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CAGGTGTGAGGACAAGAATGCAAATGGCTCTTCCTTGAGTGAAAGAA
                                                                            ATGCATACAAGGAGTCCTGAGGTGGTGATTTGGCCAGTGTTTTAACTTGTGACAAGTACT
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db_xref="taxon:9606"
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ALIGNMENTS

REFERENCE AUTHORS TITLE SOURCE ORGANISM DEFINITION ACCESSION VERSION KEYWORDS RESULT 1 BD233456 LOCUS ORIGIN FEATURES COMMENT Matches Query Match Best Local Similarity JOURNAL source 127; SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
OS Homo sapiens (human)
PN JP 2002519016-A/2
PD 02-JUL-2002
PD 02-JUL-2002
PF 18-JUN-1999 JP 2000557267
PF SEISHI KATO, TOMOKO KIMURA SSEFF PF PP PS Human protein having hydrophobic domain and DNA encoding the same Patent: JP 2002519016-A 2 02-JUL-2002; Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; BD233456.1 GI:33043226 JP 2002519016-A/2. C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N5/10,C12N15/00,C12N5/ PC 1 (bases 1 to 582) Kato,S. and Kimura,T. Human protein having hydrophobic BD233456 Homo sapiens Homo sapiens (human) BD233456 Key source Conservative Human protein having hydrophobic domain /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /organism='Homo sapiens Location/Qualifiers 88.3**%**; 96.9**%**; same 0, Location/Qualifiers
1. .582 Score 114.8; DB 6; Pred. No. 1.7e-15; 0; Mismatches 3; 582 đđ Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. domain DNA DB 6; and DNA encoding the same. Indels Length linear and DNA encoding the (human)'. PAT 17-JUL-2003 1; Gaps

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Submitted (23-APR-2002) Gillet G.,
DU VERCORS, 69367, FRANCE
Location/Qualifiers
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Mammalia; Eutheria; Primates;
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anti-apoptotic protein; NRH gene.
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                                                                           GTGCTCTCCGACAGCCCCGGCCCCACCT-GGGAGNAGTGGTGACGCTCGTGACCTTCGCA
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                           GGGACGCTGCT 130
                                                          GTGCTCTCCGACAGCCCCGGCCCCACCTGGGGCAGAGTGGTGACGCTCGTGACCTTCGCA
                                                                                                                   TCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC
                                                                                                                                    TCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC
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                                                                                                                                                                                                                                             /db_xref="GI:20338766"
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RTPFPLAFWRKQLVQAFLSCLLTTAFIYLWTRLL"
                                                                                                                                                                                                                                                                                                                                                        /codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                     function="apoptosis inhibitor"
                                                                                                                                                                                                                                                                                                                                                                                                                 gene="NRH"
                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="NRH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome="15"
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                                                                                                                                                                         Score 114.8; DB 9;
Pred. No. 1.7e-15;
0; Mismatches 3;
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Catarrhini; Hominidae;
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RESULT 4
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                             Matches 127;
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                                                                                                                                                                                                                                                                                                      193
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                          Homo sapiens (human)
Homo sapiens
                                                                    CQ752105 72
Sequence 38039 from Patent
CQ752105
CQ752105.1 GI:42387450
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Submitted (05-JUL-2000) University Women's Hospital,
46, Basel 4057, Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang,H., Holzgreve,W. and De Geyter,C.
Bcl2-L-10, a novel anti-apoptotic member of the
Bclcks apoptosis in the mitochondria death pathw
death receptor pathway 2228-2338 (2001)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa;
Mammalia; Eutheria;
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Homo sapiens Bcl-2-like protein
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                                                                                                                                                                                                                                                                          GTGCTCTCCGACAGCCCCGGCCCCACCT-GGGAGNAGTGGTGACGCTCGTGACCTTCGCA 119
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                                                                                                                                                                                      GGACGCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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/protein id="Bcl-2-like protein 10"
/protein id="AAG00503.1"
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EAGTLLERGPLYTARWKKWGFQPRLKEGEGDVARDCQRLVALLSSRLMGQHRAWLQAQ
GGWDGFCHFFRTPFPLAFWRKQLVQAFLSCLLTTAFIYLWTRLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="ovary"
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96.9%;
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Chordata;
Primates;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                          Score 114.8;
Pred. No. 1.
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                                                                                                   26 bp DNA
WO02068579.
 Craniata; Vertebrata; l
Catarrhini; Hominidae;
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pathway but not in
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                Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                       named to 887)

1 (bases 1 to 887)

Ke,N., Godzik,A. and Reed,J.C.

Rel-B, a novel Bcl-2 family member that differentially binds and regulates Bax and Bak

J. Biol. Chem. 276 (16), 12481-12484 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ke,N., Godzik,A. and Reed,J.C.
Direct Submission
Submitted (07-DEC-2000) The Burnham
Pines Rd., La Jolla, CA 92037, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens BCLB (BCLB)
AF326964
AF326964.1 GI:13898393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 887)
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fagtllergplytarwkkmgfQprlkeQegdvardCQrlvallssrlmgQhramlQaQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                     organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
                                                                                                                                                                  gene="BCLB"
                                                                                                    note="BCL2 family protein; codon_start=1
                                                                                                                                    gene="BCLB"
                                                                                                                                                                                                     map="15q21"
                                                                                                                                                                                                                       chromosome="15"
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Pred. No. 1.6e-15;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  887 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                      Boo-like"
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                                                       229 GTGCTCTCCGACAGCCCCGGCCCCACCTGGGGCAGAGTGGTGACGCTCGTGACCTTCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                        PC PR PN OS
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Kato,S. and Kimura,T.
Human protein having hydrophobic domain and DNA Patent; JP 2002519016-A 12 02-JUL-2002;
                                                                                                                                                                                                                                                                                                                      SSEEE
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Human protein having hydrophobic domain
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GGACGCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
JP 2002519016-A/12
02-JUL-2002
18-JUN-1999 JP 2000557267
SBISHI KATO, TOMOKO KIMURA
                                                                                                                                                                                                                                                                                                                                  Key
source
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                              Human
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                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                           protein having hydrophobic domain
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96.9%;
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                                                                                                                                                                    Score 114.8; DB 6
Pred. No. 1.5e-15;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (06-UUL-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (04-JUL-2001) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
98105, USA
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Burke, J., Dors, M., Fleetwood, P.,
Pate, D. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (20-FEB-2000) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S., Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R., Pate,D. and Hood,L.
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Sequencing of human chromosome 15 D15S146-D15S117 region
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AC023906
AC023906.7 GI:14595770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: leerowen@systemsbiology.org
------ Summary Statistics
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
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                                          /clone="CTD-2184D3"
/clone lib="Cal Tech Human BAC library D"
/clone lib="Cal Tech Human BAC library D"
/note="Data from overlapping clones CTD-2650P22 AC090970,
/RP11-47K1 AC016824, and RP11-430B1 was added and the
consensus was determined from CTD-2184D3 to the extent
possible"
                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="15"
note="overlap with CTD-2650P22 AC090970"
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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15 clone CTD-2184D3 map 15q21.2, complete
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Kaur,A., Madan,A., Nesbitt,R.,
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                                                                                                                                                                                                  of Washington, PO BOX 357730, Seattle
On Jun 4, 2000 this sequence version
------ Genome Center
                                                                                                                                                                                                                  Submitted (22-DEC-1999) Multimegabase Sequencing Center, of Washington, PO BOX 357730, Seattle, WA 98195, USA On Jun 4, 2000 this sequence version replaced gi:6630517
                                                                                                                                                                                                                                                                                                                              Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A. Madan, A., Nesbitt, R., Shaffer, T. and Hood, L. Sequencing of human chromosome 15 D15S146-D15S117 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 15 clone RP11-337B11 map 15q21,
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Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                                                     Contact: leerowen@systemsbiology.org
                                                                                                                                                       Center: Multimegabase Sequencing Center Center code: UWMSC
                                                                                                                                Web site: http://chroma.mbt.washington.edu/msg_www
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82012. .93287
/note="overlap with RP11-430B1 AC010674"
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/note="low quality data"
14722. .14808
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71552. .71593
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Pred. No. 7.3e-16;
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NOTE: This record contains 192 individual sequencing reads that have not been assem

assembled into

31813: contig of 832 l 31913: gap of unknown 33056: contig of 1143 33156: gap of unknown 34007: contig of 851 l 34107: gap of unknown 35320: contig of 1213 35420: gap of unknown	28691: contig of 1266 bp in 28791: gap of unknown lengt 29755: contig of 864 bp in 29755: gap of unknown lengt 30881: contig of 1126 bp in 30881: gap of unknown lengt	24296: gap of unknown 25141: contig of 845 25241: gap of unknown 26385: contig of 1144 26485: gap of unknown 27325: contig of 840 27425: gap of unknown	19774: contig of 19874 gap of contig of 20700: contig of contig of 22036: contig of 22136: gap of contig of 23123: gap of contig of 23123: contig of contig	6 11811: Contig of 806 bp in ler 1911: gap of unknown length 2 11293: contig of 1382 bp in le 13393: gap of unknown length 4 13393: gap of unknown length 14211: contig of 818 bp in ler 14311: gap of unknown length 2 14311: gap of unknown length 6 1565: gap of unknown length 6 16379: contig of 814 bp in ler 16479: gap of unknown length 17624: contig of 1145 bp in le 17624: contig of 1145 bp in le 17724: gap of unknown length 18578: contig of 854 bp in ler 18678: gap of unknown length	order in which they appear is a cing clones that may be gene-ric ing clones that may be gene-ric the sequenced to be assumed that equenced to completion. In the accession number of the sequenced to completion in the sequenced to completion in the sequenced to completion. In the sequenced to completion in the sequenced to completion in the sequenced to completion in the sequenced to completion in the sequenced to completion in the sequence s
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ACCESSION
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AY029163
                                                                                                                                                                                                                     Submitted (29-MAR-2001) Neurology Research, The Children's Hospital of Philadelphia, Abramson Research Center, Room 516 I, 3517 Civic Center Boulevard, Philadelphia, PA 19104, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         Itoh,T., Itoh,A. and Pleasure,D.
BC1-2-related protein family gene expression during oligodendroglial differentiation oligodendroglial differentiation J. Neurochem. 85 (6), 1500-1512 (2003)
                                                                                                                                                                                                                                                                                        Itoh, T., Itoh, A. and Pleasure, D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Norway rat)
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                                            /gene="Bcl2l10"
/note="Boo, Diva"
               /product="BCL2L10"
                                                                                               /gene="Bc12110"
                                                                                                                                                  /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
protein_id="AAK31792.1"
                                 codon_start=1
                                                                                                                                    db_xref="taxon:10116"
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4: contig of 1117 bp in length
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6: contig of 816 bp in length
7: gap of unknown length
8: contig of 1138 bp in length
8: gap of unknown length
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Pred. No. 3.3e-10;
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Anylebechi, V., Atleur, H., Arbucors, S., Multi, A., Anylebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baidwin, D., Bandaranaike, D., Barber, M., Barstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bhlay, C., Burch, P., Burrell, K., Calderon, E., Craderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claderon, E., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Claveland, C., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Dayola, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Dayola, M. L., Durab, R., Durbin, K., Duval, B., Eaves, K., Draper, H., Divya, K., Draper, H., Digan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Draper, H., Dispan, R., Carria, A., Garria, A., Garria, A., Garria, A., Garria, R., Garria, A., Garria, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garria, M., Gebregoorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gharray, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Harry, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Harry, Y., Havlak, P., Haddun, S.L., Hodgson, A., Hogues, M., Garcia, M., Guevara, W., Gharry, Y., Goldon, S., Uningon, A., Hogues, M., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Lordon, P., Longacre, S., Lopez, J., Loudon, P., Longacre, S., Lopez, J., Loudon, P., Mandoud, M., Malloy, K., Mangum, A., Martin, R., Martinez, E., Montemayor, J., Moore, S., McLeod, M., Mangum, A., Pal, S., Parks, K., Parks, K., Parks, K., Parks, K., P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 GACGCT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 GCTCTCCAATGACCAAGAGTTCAACTGGGGCCGCCTGGTGATGCTCCTGGCCTTCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unordered pieces.
AC111669
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Rattus norvegicus clone CH230-54I10, WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C. Allen,H., Alsbrooks,S., Amin,A., Anguiano,D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC111669.4 GI:24818904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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QIQQEHQDLFNSFRDYQGNRLELVTQMADELLSNDQEFNWGRLVMLLAFVGTLMNQDR
TVKRRRDQRNKLLLERDCYLLVSLLYNRLTGRHRSWLEAHGGWDGFCQFFKNPLFPGF
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
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Regier, M.A.,

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Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rookey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, B., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, M., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, A., Waldron, L., Walker, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wight, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:23196052.
The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (19-FBB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Direct Submission
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                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h
NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gare unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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                                                 9793
9893
118025
118125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- Genome Center
9792: contig of 9792 bp in length
9892: gap of unknown length
118024: contig of 108132 bp in length
118124: gap of unknown length
236958: contig of 118834 bp in length
237058: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _data.html).
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REFERENCE AUTHORS

TITLE JOURNAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21975 CTCCTTCCGCGACTACCAGGGCAACCGCCTGGAGCTGGTGACACAGATGGCGGATGAGTT 22034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GACGCT 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF102501 1209 bp mRNA linear AF102501
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                                                                                                                                                                  Submitted (28-OCT-1998) Pathology, Ur Catherine Road, Ann Arbor, MI 48109,
                                                                                                                                                                                                  Song, Q.Z., Kuang, Y.P., Dixit, V.M. and Vincenz, C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                        Song, Q., Kuang, Y., Dixit, V.M. and Vincenz, C.
                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 1209)
                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF102501.1 GI:4165137
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                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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clone_end:Sp6
site:EcoRI
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118125. .119133
                               map="D9"
                                                   /chromosome="9"
                                                                 /strain="B6D2 F1/J"
/db_xref="taxon:10090"
                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-54I10"
 tissue_type="ovary"
                                                                                                                  organism="Mus musculus"
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lone_end:Sp6"
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                                                                                                                                      . .1209
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238498: gap of unknown
240461: contig of 1963
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                                                                                                                                                                                  University of Michigan,
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REFERENCE
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                                                                                                                                                                                                                                                                                Inohara,N. and Nunez,G.
Direct Submission
Submitted (20-MAY-1998) Department of Pathology,
Michigan Medical School, 1500 E.Medical Dr., Ann
USA
                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1225)
Inohara,N., Gourley,T.S., Carrio,R., Muniz,M., Merino,J.,
Garcia,I., Koseki,T., Hu,Y., Chen,S. and Nunez,G.
Diva, a Bcl-2 homologue that binds directly to Apaf-1 and
BH3-independent cell death
J. Biol. Chem. 273 (49), 32479-32486 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF067660
AF067660.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus Bcl-2 homolog (Diva) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                             99047617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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/product="Bc1-2 homolog"
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                                                                                                                                            /gene="Diva"
143. .718
                                                                                                                                                                                                                                                      Location/Qualifiers
1. .1225
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/note="DIVA"
                                                                                                                                                                                                      organism="Mus musculus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="Boo"
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Pred. No. 0.16;
0; Mismatches 41
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Arbor, MI
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                                                                                                                                                           AUTHORS
TITLE
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Best Local
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                                                                 Contact: MGC help desk
                                                                                                                                                           Direct Submission
                                                                                                                                                                         Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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1225
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67.2%;
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Strauberg, I., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Generation and initial analysis of more than 15,000 full-length

human and monuse CNNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 TIGCTCTCCAAAGACCAAGACTTCAGCTGGAGCCAACTGGTGATGCTCCTGGCCTTCGCG 433
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                                                                                                                                                                                                                                                                                    Submitted (16-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus Bcl2-like 10, mRNA IMAGE:30052580), complete cds. BC052690
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cDNA Library Preparation: Yulan Piao and Minoru Ko (National Institute on Aging, NIH: http://lgsun.grc.nia.nih.gov/cDNA/)
                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Minoru K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          numan and mouse cDNA sequences
nro Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTCCTTCTGCGAAAGCCGGGGCAATCGCCTGGAGCTGGTGAAACAGATGGCAGATAAG 373
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Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 112 Row: h Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7304926.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                          h 39.2%;
Similarity 67.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Young, A.,
                                                                                  TTGCTCTCCAAAGACCAAGACTTCAGCTGGAGCCAACTGGTGATGCTCCTGGCCTTCGCG 435
                                                                                                                          GIGCTCTCCGACAGCCCCGGCCCCACCTGG-GAGNAGTGGTGACGCTCGTGACCTTCGCA 119
                                                                                                                                                                    TCCTCCTTCTGCGAAAGCCGGGGCAATCGCCTGGAGCTGGTGAAACAGATGGCAGATAAG 375
                                                                                                                                                                                                              TCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC 60
                                       GGGACGCT 127
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Bc12110"
/codon_start=1
/product="Bc12110 protein"
/protein_id="AAH52690.1"
/brotein_id="A3H52690.1"
/db_xref="GI:30851239"
                                                                                                                                                                                                                                                                                                                                                                                                                                              VTRQIQQEHQEFFSSFCESRGNRLELVKQMADKLLSKDQDFSWSQLVMLLAFAGTLMN
QGPYMAVKQKRDLGNRVIVTRDCCLIVNFLYNLLMGRRHRARLEALGGWDGFCRFFKN
PLPLGFWRRLLIQAFLSGFFATAIFFIWKRL"
                                                                                                                                                                                                                                                                                                                                                            /gene="Bc12110"
/note="BCL; Region: BCL (B-Cell lymphoma)"
/db_xref="CDD:smart00337"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="taxon:10090"
/clone="MGC:60542 IMAGE:30052580"
/tlasue_type="Egg, unfertllized, mouse"
/clone_Tib="NIA Mouse Unfertilized Egg cDNA Library
(Lona)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="LocusID:12049"
/db_xref="MGI:1330841"
/translation="MADSQDPLHGRTRRLLSDYIFFCARBPDTPBPPPTSVBAALLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="synonyms: Boo, Diva"
/db_xref="LocusID:12049"
/db_xref="MGI:1330841"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="Bcl2l10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mol_type="mRNA"
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  443
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Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                            Length 1257;
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                                                         RESULT 15
AC115880
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RESULT 14

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ACCESSION
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AC115880
AC115880.11
HTG.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:http://genome.wustl.edu
Contact: submissions@watson.wustl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-SEP-2004) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA On Sep 8, 2004 this sequence version replaced gi:50199129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-JUL-2004)
Parkway, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (20-SEP-2002)
Parkway, St. Louis, MO
3 (bases 1 to 168997)
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Wilson, R.K.
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Mus musculus chromosome 9 clone
AC133947
                                                                          Mus musculus
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Direct Submission
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4 (bases 1 to 168997)
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McPherson, J.D. and Wat
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                                                                                            AC115880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                  TTGCTCTCCAAAGACCAAGACTTCAGCTGGAGCCAACTGGTGATGCTCCTGGCCTTCGCG 166702
                                                                                                                                                                                                                                                                                                                                                                            TCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC 60
                                                                                                                                                                                          GGGACGCT 166710
                                                                                                                                                                                                                             GGGACGCT
                                                                                                                                                                                                                                                                                                    GTGCTCTCCGACAGCCCCGGCCCCACCTGG-GAGNAGTGGTGACGCTCGTGACCTTCGCA 119
                                                                                                                                                                                                                                                                                                                                           TCCTCCTTCTGCGAAAGCCGGGGCAATCGCCTGGAGCTGGTGAAACAGATGGCAGATAAG 166642
   musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="RP24-18912"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'mol_type="genomic DNA
'db_xref="taxon:10090"
'chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                          202851 bp DNA linear ROI chromosome 9, clone RP24-365N15, complete
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Pred. No. 0.072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 168997;
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RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Alden, N., Barran, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Corum, B., DeArellano, K., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Ilav, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lianders, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., McCarthy, M., Macdonald, P., Major, J., Manning, J., Mantthews, C., McCarthy, M., Macdonald, P., Major, J., J., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachungka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachungka, A., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Steinse, M., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Doley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Eardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connot, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
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Mus musculus chromosome 9, clone RP24-365N15
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Submitted (28-FEB-2004) Whitehead Institute/MIT Center for Genome
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Submitted (02-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA On Apr 2, 2004 this sequence version replaced gi:44681569. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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Center clone name: 365_N_15
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/rpt_family="B2_Mm2"
complement(3934. .40)
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site:MboI"
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clone_end:SP6"
                                                              /rpt_family="(GA)n"
7139. .7283
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7287._.7326
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chromosome="9"
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family="(GAAA)n"
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                                                           30568 TTGCTCCAAAGACCAAGACTTCAGCTGGAGCCAACTGGTGATGCTCCTGGCCTTCGCG 30627
                            120 GGGACGCT 127
                                                                            61 GTGCTCTCCGACAGCCCCGGCCCCACCTGG-GAGNAGTGGTGACGCTCGTGACCTTCGCA 119
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complement(12333...12493)

/rpt_family="BB1D7"

complement(12620...12631)

/rpt_family="TD5"

complement(12632...12757)

/rpt_family="B1F"
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complement (10978. .11186)
/rpt family="MTD"

complement / ****
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11913. .12060
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complement(10225...10356)
/rpt_family="B1_MM"
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13921 .14047
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complement (12758. .12821)
/rpt_family="ID5"
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/rpt_family="ORR1A-int"
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complement(10673...1
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9184. .9220
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This sequence represents the hydrophobic domain containing protein, clone HP00651 coding region. The sequence is isolated from a human stomach cancer call line. The HP02403 protein contains one putative transmembrane domain. The protein shows homology to the japanese quail apoptosis

Claim 3; Page 84; 117pp; English.

Novel human proteins having hydrophobic domains used diagnostic purposes.

for research and

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Abq77425 Human CGD	Adf30786 Soil meta	Abl12245 Drosophil	Abz58812 S. cinnam	Aah70552 Human cer	Adq75857 Barley ly	Ade86070 Streptomy	Abs78669 S. ghanae	Abz57164 Human met	Aaq36369 T.thermop	Adj39313 Plant cDN	Ada48367 Rice gene	Aav25925 Streptomy	Aat93095 Streptomy	Ada70199 Rice gene	Acc70866 Rice star	Acc70867 Rice star	Acc70869 Rice star	Acc70868 Rice star	Adj40034 Plant cDN	Adc07863 Rice DNA	Aba01821 Rice star	Adr01299 Mouse int	Adq91243 Mouse cDN	Adj88256 Murine IL

ALIGNMENTS

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RESULT 1
AAZ90039
Hydrophobic domain; clone HP02403; nutritional supplement; SCID; HIV; cell proliferation; immune stimulant; immune deficiency; tumour; pain; rheumatoid arthritis; insulin dependent diabetes mellitus; fertility; myasthenia gravis; haematopoiesis regulator; tissue growth; depression; anti-inflammatory; infection; bodily characteristic; ss.
                                                                                                 WPI; 2000-160665/14.
P-PSDB; AAY78802.
                                                                                                                                Kato S,
                                                                                                                                                                                 26-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                 Hydrophobic domain containing protein clone HP02403 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                       09-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                          AAZ90039;
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                                                                                                                                                                                                     18-JUN-1999;
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                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                  (SAGA ) SAGAMI CHEM RES CENT.
(PROT-) PROTEGENE INC.
                                                                                                                                Kimura T;
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RESULT 2
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AC AAD4
XX AAD47
AC AAD4
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XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX Horol
KW Creu
KW Prol
KW SCA;
KW Stro
KW SCA;
KW Gere
XX Homo
OS Homo
OX Key
FT CDS
FT CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC humans and animals Suggested activities include nutritional activity
CC (nutritional source or supplement); cytokine and cell
CC proliferation/differentiation activity; immune stimulating (e.g. as
CC vaccines) or suppressing activity (e.g. to treat various immune
CC deficiencies such as SCIDS or HIV, connective tissue disease, systemic
CC lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary
CC inflammation, Guillain-Barre syndrome, autoimmune pulmonary
CC inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin
CC dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease
CC and autoimmune inflammatory eye disease, as well as asthma, allergies and
CC organ transplantation); haematopoiesis regulating activity (e.g. in
CC treatment of myeloid or lymphoid cell deficiencies); tissue growth
CC activity; (e.g. wound healing and tissue repair, ulcers, burns,
CC periodontal disease); activin/inhibin activity; chemotactic/chemokinetic
CC activity; haemostatic and thrombolytic activity (e.g. treating
CC tumour inhibition activity. The polymucleotides are also stated to be
CC useful for gene therapy. Other activities include inhibiting infections
CC malaria); effecting blorhythms or caricadic cycles; enhancing fettility;
CC treatment of depression; treatment of pain; hormonal or endocrine
CC of the profesion
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Best Local :
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                                                                                                                                                                                                   Human; Bcl-2; Bcl-B; therapy; apoptosis; cell degenerative disorder; proliferative disorder; muscle degeneration; Alzheimer's disease; CJD; Creutzfeldt-Jacob's disease; Mchado-Joseph disease; MJD; transgenic; Parkinson's disease; Huntington's disease; HD; spinocerebellar ataxia; SCA; dentatorubropallidoluysian atrophy; DRPLA; Kennedy's disease; stroke; ischaemia; head trauma; neoplasia; anticonvulsant; vulnerary; nootropic; neuroprotective; cytostatic; immunosuppressive; vasotropic; cerebroprotective; autoimmune disorder; chromosome 15; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Bcl-B
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                          /product= "Human Bcl-B
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96.9%;
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Matches 127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human member of Bcl-2 family Bcl-B protein and its corresponding nucleic acid. Bcl-B is useful in treating a subject having or at risk of a disorder associated with apoptosis, such as cell degenerative or proliferative disorder like neural or muscle degeneration, e.g. Alrheimer's disease, Creutzfeldt-Jacob's disease (CJD), Machado-Joseph disease (MJD), Parkinson's disease, Huntington's disease (HJD), spinocerabellar ataxias 1, 2 and 6 (SCA-1, - 2 and -6), dentatorubropallidoluysian atrophy (DRPLA), Kennedy's disease, stroke, ischaemia, head trauma, neoplasia, autoimmune disorder or fibrotic condition. The transgenic animals are used as in vivo models to study apoptosis and potential therapies for apoptosis. The present sequence is human Bcl-B DNA. Bcl-B gene is located at chromosome 15
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P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated or recombinant Bcl-B nucleic acids and polypeptides, for treating a disorder associated with apoptosis, such as cell degenerative or proliferative disorder e.g. cancer, Alzheimer's disease or Parkinson'
                                                        cell proliferation; immune stimulant; immune deficiency; tumour; pain; rheumatoid arthritis; insulin dependent diabetes mellitus; fertility; myasthenia gravis; haematopoiesis regulator; tissue growth; depression;
                                                                                                         Hydrophobic domain;
                                                                                                                                       Hydrophobic domain containing
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07-FEB-2002;
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                                                                                                                                                                                                                                   standard; cDNA; 1168
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2002US-00071174.
                                                                                                                                                                      (first entry
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                                                                                          clone HP02403; nutritional immune stimulant; immune de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.3%;
96.9%;
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Pred. No. 1.6e-19;
D; Mismatches 3
                                                                                                                                       protein clone HP02403 nucleotide sequence.
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Homo sapiens

WO200000506-A2

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CC vaccines) or suppressing activity (e.g. to treat various immune CC deficiencies such as SCIDS or HIV, connective tissue disease, systemic CC lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary CC inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin CC dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease CC and autoimmune inflammatory eye disease, as well as asthma, allergies and CC organ transplantation); haematopoiesis regulating activity (e.g. in CC treatment of myeloid or lymphoid cell deficiencies); tissue growth CC activity; haemostatic and thrombolytic activity; chemotactic/chemokinetic CC activity; haemostatic and thrombolytic activity (e.g. treating CC haemophilias); receptor/ligand activity; anti-inflammatory activity; and CC tumour inhibition activity. The polymucleotides are also stated to be CC caused by bacteria, fungi, viruses and other parasites (e.g. Hepatitis, CC malaria); effecting bodily characteristics such as, e.g. weight, colour, CC treatment of depression; treatment of pain; hormonal or endocrine CC cativity. The polymucleotides are also stated of colour, Skin, effecting bodily characteristics such as, e.g. weight, colour, CC treatment of depression; treatment of pain; hormonal or endocrine CC of the protein
                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1168 BP; 276 A; 312 C; 300 G; 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell proliferation/differentiation activity; immune stimulating (e.g. as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 92-94; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic purposes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kato S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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DB; AAY78802.
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Similarity 96.9%;
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                                                                                                                                                                                             GTGCTCTCCGACAGCCCCGGCCCCACCT-GGGAGNAGTGGTGACGCTCGTGACCTTCGCA 119
                                                                                                                                                                                                                                                                                               TCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC
                                                                                                                                                                                                                                                               TCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC
GGGACGCTGCT 299
                                                           GGGACGCTGCT 130
                                                                                                                                 GTGCTCTCCGACAGCCCCGGCCCCACCTGGGGCAGAGTGGTGACGCTCGTGACCTTCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Pred. No. 1.6
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RESULT 4

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ABK41913
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06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
                                                                                                                                                                        23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                                                             18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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14-AUG-2000;
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26-JUL-2000;
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2000US-020515P.
2000US-0214886P.
2000US-0214886P.
2000US-0214886P.
2000US-021684P.
2000US-021684P.
2000US-021689P.
2000US-0224519P.
2000US-0225213P.
2000US-0225213P.
2000US-0225213P.
2000US-0225268P.
2000US-0225268P.
2000US-0225758P.
2000US-0225758P.
2000US-0225758P.
2000US-0225758P.
2000US-0225758P.
2000US-0225739P.
2000US-0225739P.
2000US-0225739P.
2000US-0226888P.
2000US-0229343P.
2000US-0229343P.
2000US-0229343P.
2000US-0229343P.
2000US-023943P.
2000US-0231443P.
2000US-0231444P.
2000US-0231444P.
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2000US-0180628P
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ADBS950A
ADBS950A
AC ADBS
XX ADBS
XX ADBS
XX Cytc
COIN
XX Cytc
KW Cytc
KW Cytc
KW Cytc
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Best Local Sim:
Matches 105;
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08-DEC-2000

11-DEC-2000

11-DEC-2000

11-DEC-2000
                      gene therapy; ds; connective tissues disorder; rheumatoid arthritis; systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer cancer metastasis; neeplasia; leukaemia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; cardiovascular disease; atherosclerosis; myocarditis; cardiopulmonary bypass complication; autoimmune disease; multiple sclerosis; allergic reaction; asthma; rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel human connective trissue related polypeptides (AAU86435-AAU86923) and the polypucleotide (cDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polypucleotide sequences of the invention are also useful igene therapy. ABK41613-ABK42101 represent cDNA sequences encoding the novel human connective tissue related polypeptides. Note: The sequence data for this patent did not form part of the printed specification, by was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                       antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritic; antiinflammatory; antiallergic; antiasthmatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding novel connective tissue associated used in diagnosing, preventing, treating or ameliorating as cancer or rheumatoid arthritis.
     gastrointestinal disorder;
                                                                                                                                                                                                                                                                                                     cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2003
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                                                                                                                                                                                                                   nephrotopic; virucide; fungicide;
                                                                                                                                                                                                                                                                                                                                                        Connective tissue related polynucleotide #301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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2000US-0251719P.
2000US-0251479P.
2000US-0251868P.
2000US-0251868P.
2000US-0251869P.
2000US-0251989P.
2000US-0251990P.
2000US-0251990P.
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                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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        inflammatory bowel
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antibacterial; antiparasit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
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a disorder such
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2000US-0232398 2000US-02323063P 2000US-0233401P 2000US-0233063P 2000US-0233499P 2000US-023499P 2000US-0235484P 2000US-0235836P 2000US-0235836P 2000US-023632P 2000US-023632P 2000US-023632P 2000US-023632P 2000US-023632P 2000US-023632P 2000US-023632P 2000US-023632P 2000US-024682P 2000US-0241786P 2000US-0241786P 2000US-024677P 2000US-024921P
14-SEP-2000
14-SEP-2000
14-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
20-CCT-2000
21-CCT-2000
21-CCT-2000
20-CCT-2000
21-CCT-2000
21-CCT-2000
21-NOV-2000

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RESULT 6
AAH47022
ID AAH4
XX AAH4
XX AAH4
XX AH4
XX BC1
DT 29-C
XX BC1
DE Huma
XX Huma
XX Homo
CX Hom
CX Homo
CX Homo
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The polypeptide or polynucleotide encoding connective tissue antiques (CTA). The polypeptide or polynucleotide is useful for preventing, treating, or ameliorating medical conditions in a mammal. The connective tissue polypeptides, polynucleotides and antibodies are particularly useful for treating, preventing and/or prognosing disorders of connective tissues (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus, scleroderma, or Sjogren's syndrome), cancers, cancer metastases and/or neoplasias (e.g. leukaemia), neurodegenerative disorders (e.g. Alzheimer's disease, or Parkinson's disease), cardiovascular diseases (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass complications), autoimmune diseases (e.g. systemic lupus erythematosus, autoimmune diseases (e.g. systemic lupus erythematosus, complications),       09-AUG-2001.
                                                               WO200157060-A1
                                                                                                                                                                                                                                                                                                                                                                        immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bcl-2-like polypeptide; autoimmune disorder; allergy; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Bcl-2-like polypeptide encoding cDNA (clone HLIBE40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH47022 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated nucleic acid molecule (I), which comprises a sequence that is at least 95 % identical to a connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 311; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New connective tissue-related polypeptides and polynucleotides, useful for treating, preventing and/or prognosing e.g. disorders of connective tissue (e.g. rheumatoid arthritis), cancers, cancer metastases and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                        respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Sim.
                                                                                                                                                                                                                                                                                                           sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGCCCCACCTGGGCAGAGTGGTGACGCTGGCAGGGACGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGTGCTCTCCGACAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGCCCCACCTGGGAGNAGTGGTGACGCTCGTGACCCTTCGCAGGGACGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACGCGTCCGGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGTGCTCTCCGACAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arthritis, or multiple sclerosis), allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2000US-0251989P.
; 2000US-0251990P.
; 2000US-0254097P.
; 2001US-0259678P.
; 2001US-00764847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                     product= "Bcl-2-like polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,MS
                                                                                                                            note≈ "gene No.
                                                                                                                                                                                                                                                                                                                                                                           antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 100.8;
Pred. No. 5e-1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SC
                                                                                                                                                                                                                                                                                                                                                                                                        antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5e-16;
                                                                                                                                                                                                                                                                                                                                                                    therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                        immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     548;
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RESULT 7
ABQ44403
ID ABQ4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC 2-like polypeptides (PEP1). The NAM1 and PEP1 may be used in the CC prevention, diagnosis and treatment of diseases associated with CC inappropriate Bc1-2-like polypeptides' expression. The NAM1 may be used CC to produce the soluble Bc1-2-like polypeptides by standard recombinant CC methodolgy. The polypeptides may also be used as antigens in the production of antibodies against Bc1-2 and in assays to identify CC modulators of Bc1-2 expression and activity. The anti-Bc1-2 antibodies and antagonists may be used to down regulate expression and activity. The anti-Bc1-2 antibodies CC and antagonists may also be used as diagnostic agents for detecting the presence of Bc1-2 polyps in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). Disorders that may be prevented, diagnosed CC immunosorbant assay (ELISA). Disorders that may be prevented, diagnosed CC and/or treated by the above methods include, immunodeficiencies (e.g. a cC gammaglobulinemia and B cell lymphoproliferative disorder), autoimmune CC disorders (e.g. rheumatoid arthritis and Grave's disease), allergic CC reactions, inflammations, respiratory diseases and cardiovascular CC disorders (a full list of disorders is given in the specification). The present sequence represents a human Bc1-2-like polypeptide encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                     Human; cytosine methylation; 5'-Cpg-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides nucleic acid molecules (NAM1) encoding -2-like polypeptides (PEP1). The NAM1 and PEP1 may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2000;
07-FEB-2000;
                                                                                                                                                                                                           Oligonucleotide
                                                                                                                                                                                                                                                                                                                    ABQ44403 standard; DNA; 874 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding preventing, diagnosing
                                                                                                                                                                                                                                              12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2001; 2001WO-US003080
                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                          89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 GCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGTGCTCTCCGACAGCCCCCGGCCCCACCT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          GGGGCAGAGTGGTGACGCTCGTGACCTTCGCAGGGACGCTGCT 103
                                                                                                                                                                                                                                                                                                                                                                                                                               -GGGAGNAGTGGTGACCTTCGTGACCTTCGCAGGGACGCTGCT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGTGCTCTCCGACAGCCCCGGCCCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 276; 285pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      522 BP; 102 A; 148 C; 154 G; 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0179487P.
2000US-0180697P.
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                           for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.8%;
96.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human Bcl-2-like polypeptides, useful for and/or treating.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٦,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 86.8; DB 4.
Pred. No. 1.6e-12
                                                                                                                                                                                                           cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                           methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 522;
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WO200218632-A2

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RESULT 8
ABQ44402/c
ID ABQ4444
XX ABQ444
AC ABQ444
XX DT 12-JUL
XX Oligon
XX DE Oligon
XX Human;
KW drug;
KW gastro
KW SNP; C
XX
OS Homo 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, CC of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers and the CC degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of CC oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central canders, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation CC status of many C residues to be determined simultaneously. ABQ13410-CC ABQ54121 represent genomic DNA sequences used to illustrate the method CC disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                       drug; side effect; cancer; central ner
gastrointestinal; respiratory system;
SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining the degree of cytosine methylation in genomic DNA, useful fidiagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                             Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                 Oligonucleotide for detecting cytosine methylation SEQ ID
                                                                                                                                                                      12-JUL-2002
                                                                                                                                                                                                                                                ABQ44402 standard; DNA; 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; 56pp + Sequence Listing; 56pp; German.
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05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                              AAAACGCTACT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGCTCTCCGACAGCCCCGGCCCCACCTGGGA-GNAGTGGTGACGCTCGTGACCTTCGCA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCGCCTACCTCGGCTACCCCCGGGAACCGCTTCGAGCTGGTGGCGCGCTGATGGCGGGATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                GGGACGCTGCT 130
                                                                                                                                                                                                                                                                                                                                                                                                                     GTACTCTCCGACACCCCGACCCCACCTAAAACAAAATAATAACGCTCGTAACCTTCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCGCCTACCTCGACTACCCCCGAAAACCGCTTCGAACTAATAACGCTAATAACGAATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 374 A; 291 C; 90 G; 119 T; 0 U; 0 Other;
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2000DE-01044543.
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                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.3%;
77.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 73.2; DB 6;
Pred. No. 4.1e-09;
0; Mismatches 29
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                                                        rvous system; cardi
single nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                          polymorphism;
                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ۲.
                                                                                                                                   30993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400
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Homo sapiens

12-JUL-2002

(first entry)

ABQ44404

standard; DNA;

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; Oligonucleotide for detecting cytosine methylation SEQ ID NO 30995.

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RESULT 9
ABQ44404
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                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpC-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CDNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on CC the amplicon. From the ratio of labels hybridised to the two classes of CC oligomers, the degree of methylation is calculated. The method is used in for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central CC nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms CC (SNP's); and (ii) for differentiation of cell or tissue types and for civestigating cell differentiation of cell or tissue types and for crows from the crowders of be determined simultaneously. ABQ13410-CC Rap54121 represent genomic DNA sequences used to illustrate the method CC disclosure of the invention
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 101; Conserv
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                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; 56pp + Sequence Listing; 56pp; German.
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05-SEP-2000;
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                                                                         AAAACGCTACT
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                                                                                                                                             GTACTCTCCGACACCCCGACCCCACCTAAAACAAAATAATAACGCTCGTAACCTTCGCA
                                                                                                                                                                       GTGCTCTCCGACAGCCCCGGCCCCACCTGGGA-GNAGTGGTGACGCTCGTGACCTTCGCA 119
                                                                                                                                                                                                                                                    TCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC
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                                                                                                           GGGACGCTGCT 130
                                                                                                                                                                                                                      TCCGCCTACCTCGACTACCCCGAAAACCGCTTCGAACTAATAACGCTAATAACGAATTCC
                                                                                                                                                                                                                                                                                            Conservative
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2000DE-01044543
                                                                                                                                                                                                                                                                                                                                                               119 A; 90 ·C;
                                                                                                                                                                                                                                                                                                         56.3%;
77.1%;
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                                                                                                                                                                                                                                                                                          Score 73.2; DI
Pred. No. 4.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 291 G; 374 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                   .2; DB 6;
4.1e-09;
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                                                                                                                                                                                                                                                                                            Indels
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RESULT 10
ABQ44405/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel method for determining the degree of cmethylation of a particular cytosine in a motif 5'-CpG-3', present in a cytosine (C) but not methylated C, to uracil, then part of the genomic Cytosine (C) but not methylated C, to uracil, then part of the genomic ChA that contains the target C is amplified to form a labeled amplicon. CT he amplicon is hybridised to two classes, each with at least one member, CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligoners and the cC degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of cligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs cand of a wide range of diseases, e.g. cancer, disorders of the central construing, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (CC garticularly by detecting mutations or single nucleotide polymorphisms convestigating cell differentiation. The method allows the methylation convestigating cell differentiation. The method allows the methylation convestigating cell differentiation. The method allows the methylation convestigating cell differentiation of cell or tissue types and for convestigating cell differentiation of cell or tissue types and for convestigating cell differentiation. The method allows the methylation convestigating cell differentiation of cell or tissue types and for convestigating cell differentiation of cell or tissue types and for convestigating cell differentiation of cell or tissue types and for convestigating cell differentiation of cell or tissue types and for convestigating cell differentiation described in the method for determining the degree of cytosine methylation described in the convertion.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                   ABQ44405
                                                          ABQ44405 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; 56pp + Sequence Listing; 56pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons
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05-SEP-2000;
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gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemically treated DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                          GGGACGCTGCT 130
                                                                                                                                                                                                                                                    GTGTTTTTCGATAGTTTCGGTTTTATTTGGGGTAGAGTGGTGACGTTCGTGATTTTCGTA
                                                                                                                                                                                                                                                                                  GIGCTCTCCGACAGCCCCGGCCCCACCT-GGGAGNAGTGGTGACGCTCGTGACCTTCGCA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piepenbrock C,
                                                                                                                                                                   GGGACGTTGTT
                                                                                                                                                                                                                                                                                                                                    TTCGTTTATTTCGGTTATTTCGGGAATCGTTTCGAGTTGGTGGCGTTGATGGCGGATTTC
                                                                                                                                                                                                                                                                                                                                                                         rcccctaccrccccrccccccccaacccccrccaaccrccrccarccccrcarccccaarrcc
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 144 A; 90 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000DE-01043826.
2000DE-01044543.
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71.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                     36;
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                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a Genomic sample of DNA. The sample is treated chemically to convert CC Cytosine (C) but not methylated C, to uracil, then part of the genomic CDNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, CC of oligonuclectides and/or peptide-nucleic acid (PNA) oligoners and the CC degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of coligoners, the degree of methylation is calculated. The method is used configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately configurately con
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; 56pp + Sequence Listing; 56pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-SEP-2000; 2000DE-01043826
05-SEP-2000; 2000DE-01044543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide
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414
                                                                                                                                                                                         534 TTCGTTTATTTCGGTTATTTCGGGAATCGTTTCGAGTTGGTGGCGTTGATGGCGGATTTC
                                                                                                                                          61
                                                                                                                                                                                                                                        _
                                                                                                                                                                                                                                                                                       94;
                                               GGGACGCTGCT 130
                                                                                                                      GTGCTCTCCGACAGCCCCGGCCCCACCT-GGGAGNAGTGGTGACGCTCGTGACCTTCGCA 119
                                                                                                                                                                                                                                                                                                                                                                                874 BP;
                                                                                           GTGTTTTTCGATAGTTTCGGTTTTATTTGGGGTAGAGTGGTGACGTTCGTGATTTTCGTA
                                                                                                                                                                                                                    TCCGCCTACCTCGGCTACCCCCGGGAACCGCTTCGAGCTGGTGGCGGCTGATGGCGGATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piepenbrock C,
GGGACGTTGTT 404
                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                320 A; 320 C; 90 G; 144 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                           47.7%;
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                                                                                                                                                                                                                                                                                  Score 62; DB
Pred. No. 2.6e
0; Mismatches
                                                                                                                                                                                                                                                                                       0,
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                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                              .6e-06
                                                                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                                                                                                                               Length 874
                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                       Gaps
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RESULT 11

415

475 60

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consen rrom sequence or ys numan probes and 2046 mouse probes. An array consuse or human sample containing nucleic acid, by contacting the array cuth the sample under conditions allowing selective hybridisation, and compared to produce an expression profile of a first labelled sample to the array to groduce an expression profile. The array is also useful for determining an expression profile of a first labelled sample containing nucleic acid crelative to a second, differently labelled sample containing nucleic acid for determining an expression profile diagnostic of an energy-metabolism-related physiological condition. An array of the invention is useful for determining mitochondrial biology gene expression profiles of organisms, such physiological conditions, the invention is useful for determining mitochondrial biology gene expression profiles of such organisms, which are useful for determining expression profiles of such organisms, which are useful for determining expression profiles of identifying biochemical conditions, genes, and mutations involved in such physiological conditions, involved in such physiological conditions, conditions, genes, and creating and/or monitoring the efficacy of such therapies, and creating and identifying animal models of human cenergy metabolism-related physiological conditions. An array is also useful for defining expression signatures or profiles for mitochondrial conditaitive phosphorylation (OXPHOS) dysfunction, oxidative stress, cappitosis and aging. An array of the invention contains probes of genes not previously recognised to participate in mitochondrial biology. The sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA colors useful for monitorial biology. The sequences used to make the probes of the invention. Some sequences are not present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905, cappides and 2643.
Array containing probes for genes involved in mitochondrial biology, useful for determining mitochondrial biology gene expression profiles use in diagnosing pathologies and identifying biochemical pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; mouse; array; mitochondrial; hybridisation; energy-metabolism; mitochondrial disease; oxidative phosphorylation dysfunction; oxidative stress; apoptosis; aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a gene involved in mitochondrial biology. The array comprises two or more isolated nucleic acid molecules or spots, each molecule having a sequence chosen from sequence of 994 human probes and 2046 mouse probes. An array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-2001;
31-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel array comprising at least two isolated nucleotide molecules, each molecule having a sequence capable of uniquely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 1910; 201pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wallace
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse mitochondrial DNA sequence
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         A cDNA clone (AAT33800) codes for murine interleukin-17 receptor (IL-17R) (AAW04184), a type I transmembrane protein. A cDNA library of murine thymoma EL4 cells was used to transform CV1/EBNA cells and the prods. were screened for binding to a fusion between the Fc region of human IgG1 (see also AAW02305) and the viral IL-17 homologue HVS13 (AAW02387). A positive clone contained a 3.2 kb insert that included the IL-17R open recombinant IL-17R in transformed host cells or to transfect a tissue or organ as a means of suppressing graft rejection. It was also used to identify a cDNA clone (AAT33801) coding for human IL-17R (AAW04185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      graft
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                                                                                                                                                    Claim 1; Page 25-29;
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07-AUG-1995;
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graft rejection; inflammation; therapy; ss.
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This cDNA sequence codes for mouse full-length interleukin-17 (IL-17) receptor (see AAW61271). It can be used for the production of recombinant IL-17 receptor polypeptides, especially a soluble polypeptide comprising the signal peptide and extracellular domain of murine IL-17 receptor, in prokaryotic or eukaryotic (for glycosylated products) expression systems. A claimed method for reducing the amount of nitric oxide produced by a cartilage associated cell comprises contacting the cell receptor, especially soluble murine or human (see AAW61272) IL-17 receptor, IL-17 is known to stimulate nitric oxide production from cartilage-associated cells in individuals with osteoarthritis. Inhibitors
                                                                                                                                                                                                                                                                      Disclosure; Page 20-24; 41pp; English.
                                                                                                                                                                                                                                                                                                                   Reducing nitric oxide production by cartilage associated cells contacting cells with soluble interleukin-17 receptor, useful to osteoarthritis and auto-immune and inflammatory diseases.
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Pred. No. 5.4;
0; Mismatches
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ease; inflammation; therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of nitric oxide production, such as soluble II-17 receptor, may therefore be useful to ameliorate the effects of nitric oxide in osteoarthritis as well as in other disease conditions in which nitric oxide plays a role, e.g. autoimmune and inflammatory diseases
                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                             IL-17R; murine; interleukin-17 receptor; immunoregulator; inhibitor;
T cell proliferation; T cell activation; organ; graft; rejection;
autoimmune disease; allergy; asthma; treatment; inflammatory disease;
                  Disclosure;
                                              treating
                                                                             P-PSDB;
                                                                                                          Spriggs
                                                                                                                                                 23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                               21-MAR-1996;
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                                                                                                                                                                                                                                                                    sig_peptide
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                                      ng e.g. organ or or inflammatory
                                                                                                                                                                                                                                                                                                                                                    proliferation;
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                                                                              AAW92408
                                                                                                                               IMMUNEX
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                                      interleukin-17 receptor DNA -
e.g. organ or graft rejection,
r inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; cDNA to mRNA; 3288
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                  Col 19-26;
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214. .2712
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95US-00538765.
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121. .213
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Pred. No. 5.4;
0; Mismatches
                  English.
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                                                                                                                                                                                                                                                                                                                                                    immunogen;
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disease, all
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This

sequence encodes a murine interleukin-17 receptor (IL-17R). IL-17R

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RESULT 15
AAA51987/c
ID AAA519
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XX AAA519
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XX Murine
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XX IL-17R
KW HSV13;
KW Anti-a
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07-AUG-1995;
21-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine interleukin-17 receptor coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-2000
Regulating, treating or preventing immune or inflammatory response mammal, especially organ or graft rejection, allergy or asthma, con
                                                                                                                                                                                                                                                                                                                                                                                          11-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                             08-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             II-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri; HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA51987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA51987 standard; cDNA to mRNA; 3288
                                                                                                                                                               Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6100235-A.
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                                                                                  2000-548298/50.
DB; AAY97130.
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Similarity 55.0%;
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95US-00538765.
96US-00620694.
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Security Fill Reference: 38 10(15849) B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 4478
LENGTH: 1704
TYPE: DNA
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  APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus x.
FILE REFERENCE: 38-10(15849)B
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Matches 70
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US-09-711-205A-1
US-09-902-40-879
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LENGTH: 28172
TYPE: DNA
ORGANISM: Myxococcus xanthus
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                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 3288 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 16825
                                                                                                            NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 01
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 21 MAR CLASSIFICATION: 435
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STATE: WA
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                                                                                              TELEPHONE:
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l Similarity 56.0%;
70; Conservative
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nucleic acid
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                                                                                              (206) 587-0430
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                                                                                                                                                                                                                                                            USSN 08/410,535
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Patent No. 6072033
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Best Local Similarity
                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410
FILLING DATE: 23 MARCH 1995
ATTORNEY/ACENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REGISTRATION NUMBER: 34,695
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USS:
FILING DATE: 21 MARCH 1:
APPLICATION NUMBER: USS:
FILING DATE: 7 AUGUST 1:
                  TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System
SOFTWARE: Microsoft Word for Apple, Versi
CURRENT APPLICATION DATA:
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APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 607:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE CHARACTERISTICS:
                                                                      REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
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LOCATION:
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TOPOLOGY: linear
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STRAIN: HVS13 receptor
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                                                      TELEPHONE:
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                                                      (206) 587-0430
                                                                                                                                                                                                                    7 AUGUST 1995
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No. 6072033el Receptor That Binds IL-17
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                                                                                          2617-B
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MOLECULE TYPE:

TOPOLOGY:

linear

cDNA to mRNA single

STRANDEDNESS: LENGTH:

nucleic acid

3288 base pairs

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US-09-022-696-1/c
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APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA;
APPLICATION NUMBER: USS
FILING DATE: 23 MARCH 1
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                    ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 7.5.5
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CURRENT APPLICATION DATA:
US/09/022,696
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APPLICATION NUMBER:
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LOCATION:
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CLASSIFICATION:
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121..2715
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                                                                                                                        USSN 08/410,535
CH 1995
                                                                                                                                                                                                          08/620,694
                                     2617-B
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RESULT 6
US-08-978-773-1/c
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                                               INFORMATION FOR SEQ ID NO:
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                                                                                                                           APPLICATION NUMBER: USSN 6
FILING DATE: 27 NOVEMBER 1
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia An
REGISTRATION NUMBER: 34,69
SEQUENCE CHARACTERISTICS:
LENGTH: 3288 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Va
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,773
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Method
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                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
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LOCATION:
                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mouse
STRAIN: HVS13 receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                              TELEPHONE:
                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GTGCTCTCCGACAGCCCCGGCCCCACCTGGGAGNAGTGGTGACGCTCGTGACCTTCGCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCGCCTACCTCGGCTACCCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunex Corporation
                                                                                (206) 587-0430
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55.0%;
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                                                                                                                      34,693
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1996
                                                                                                                 2623-A
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STRANDEDNESS: sin

single lear cDNA to mRNA

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Sequence 1, Application.

Sequence 1, Application.

Patent No. 6096305

Patent No. 6096305

Patent No. 6096305

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17

TO SROUENCES: 10
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                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System
SOFTWARE Microsoft Word for Apple, Versi
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
   CLONE: IL-17 receptor
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ORGANISM: Mou
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                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 5. Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                        APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
                               NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
                                                                                                      FILING DATE: 2 CLASSIFICATION:
                                                                                                                    APPLICATION NUMBER: USSN 01
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98101
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121..2712
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(206)587-0430
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55.0%;
                                                                                                                                        USSN 08/410,535
                                                                                                                                                                                                                                                                                                                  US/09/022,253
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COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
COMPUTER: Microsoft Word for Apple, Version 6.0..
SOFTWARE: Microsoft Word for Apple, Version 6.0..
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/620 for
FILING DATE:
CLASSIFICATION NUMBER: 08/620 for
FILING DATE:
CLASSIFICATION NUMBER: 08/620 for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILLING DATE: 23 MARCH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO ORIGINAL SOURCE:
              ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Spriggs, APPLICANT: Fanslow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
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Local Similarity 55.0%;
les 71; Conservative
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                               51 University Street
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                                                                                    23 MARCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhengbin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 6100235el Receptor That Binds IL-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Melanie
William
                                                                                                    USSN 08/410,535
                                                                                    1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ب</u>
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2617-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36.8; DB Pred. No. 0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3288;
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TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:

TELEPHONE: (206)587-0430

TELEPHONE: (200)

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US-09-022-259-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09022259
Patent No. 6191104
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.3%;
Best Local Similarity 55.0%;
Matches 71; Conservative
                                                                                                      APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE:
                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Apple, Version 6
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: NO. 6191104el Receptor That Binds IL-17
         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                  STREET: 51 Uni
CITY: Seattle
                                             FILING DATE:
                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                       COUNTRY:
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LOCATION:
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STRAIN: HVS13 receptor
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Perkins, Patricia Anne
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                                            23 MARCH 1995
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                                                          USSN 08/410,535
                                                                                                                                                                                US/09/022,259
                                                                                                                    08/620,694
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Pred. No. 0.
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US-09-022-257-1/c
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Patent No. 6197525
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                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206)
INFORMATION FOR SEQ ID NO:
                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06
PILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDN
HYPOTHETICAL: NO
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,257
           PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 0
FILING DATE: 23 MARCH 1995
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ORGANISM: Mouse
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REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
CLASSIFICATION:
                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                          CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3288 base pairs
TYPE: nucleic acid
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51 University Street
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No. 6197525el Receptor That Binds IL-17
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                           USSN 08/410,535
                                                                                          08/620,694
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                                                                                                                                                                                 Version 6.0.1
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09549679 Patent No. 6680057 GENERAL INFORMATION:
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LENGTH: 3288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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ORGANISM: Mou
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TELECOMMUNICATION INFORMATION:
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                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     AFFILE OF INVENTION: No. 6680057el Receptor That Binds IL-17
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                                                               PRIOR
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                                                            APPLICATION NUMBER: US/09/549,679
ETILING DATE: 14-Apr-2000
CLASSIFICATION: CURNOWN>
R APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGACGCTGC 129
APPLICATION NUMBER: USSN 08/410,535 FILING DATE: 23 MARCH 1995
                              APPLICATION NUMBER: 08/620,694 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCCTCGGC 2424
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ER: 2617-B
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Pred. No. 0.
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                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 6511
LENGTH: 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6511, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
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                                                                                                                             Matches
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                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
FITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                              TYPE: DNA ORGANISM: Myxococcus xanthus
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INFORMATION FOR SEQ ID NO: 1:
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SEQUENCE DESCRIPTION: SEQ ID NO:
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63 GCTCTCCGACAGCCCCGGCCCCACCTGGGAGNAGTGGTGACGCTCGT 109
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                                                                                                                             61;
                                                                                          3 CGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGT 62
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LOCATION:
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                                                        TCCTCCTCCGTGAGCCACTCGGGGGGGCTGCGGGGAGCTCCTGGAGATGTAGCCCTGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mouse
STRAIN: HVS13 r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 3288 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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55.0%;
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                                                                                                                                              26.2%;
57.0%;
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                                                                                                                                              Score 34; DB Pred. No. 2.8;
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                                                                                                                             Mismatches
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                                                                                                                                                                 DB 4;
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                                                                                                                                                               Length 1482;
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1218 GCTGAGCACCGTCCCGGGCGGCGGCTGGGAGGAGGATGAGCGGCACCT 1264

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NESULT 15
US-08-658-003-29
; Sequence 29, Application US/08858003
; Patent No. 6060234
                                                                                                                                                                                                                                                                                                                                                    ; LENGTH; 3191
TYPE; DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13105
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US-09-270-767-13105
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; ORGANISM: Myxococcus xanthus
US-09-902-540-472
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 472
LENGTH: 2581
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13105
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                          Query Match
Best Local
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Patent No. bass.
Patent INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 26.2%; ocal Similarity 57.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1219
                                                                                                                                                                                               476 CCGCTTCCAGGAGAGCAAAAACGAGCTGGATTCGCTGCTCACGGATGAGGCGCTGTCCAA 535
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                                                                                                                                                       72 CAGCCCCGGCCCCACCTGGG 91
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                                                                                                                                                                                                                                                                        l Similarity
50; Conserv
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                                                                                                                    CTGCCCCGTGCTCATATTGG
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                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 3;
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Search completed: June 7,
Job time : 42.4159 secs
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                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1010 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 1
FILING DATE: 16-MAY-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Dianne Casuto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kakavas, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (847)-938-3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP:
                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: P-4
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                      556 GGGGTGCACGCCCGGCCGATCCCCGGCGTCGACACGGCGGGCCACTCG 603
                                                                                                                                           496 TGCGCCGTCGCAGGCGACCCGGAGGCGCTGGCCGAACTGGTGGCGCTGCTGACCGGTGAG 555
                                                                                                       61 GTGCTCTCCGACAGCCCCGGCCCCACCTGGGAGNAGTGGTGACGCTCG 108
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100 Abbott Park Rd.
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nilarity 55.6%;
Conservative
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                   2005, 18:17:15
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BER: 4952.US.P2
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                                                                                                                                                                                                            Score 31.8; DI
Pred. No. 11;
0; Mismatches
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                                                                                                                                                                                                                                              Length 1010;
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Database :
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                June 7, 2005, 06:21:09 ; Search time 122.203 Seconds (without alignments) 6090.078 Million cell updates/sec
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Listing first 45 summaries
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/cgn2_6/ptodata/1/pubpna/PCT_N
/cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10 NEW PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US11A PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60 NEW PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                                                                                                                                                                              m2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
m2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/US0A_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
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6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	- ° F		Query Match 88.3	Query Match Length DB	DB	ID 6 US-10-071-174-1	Description Sequence 1, Appli
	21	114.8 100.8	88.3 77.5	887 548	9 16	16 US-10-071-174-1 9 US-09-764-847-311	ທ
	w	100.8	77.5	548	14	US-10-092-154-311	
	4.	86.8	66.8	522	ø	US-09-912-599-3	Sequence 3, Appli
ი	u	73.2	56.3	874	20	US-10-363-345A-30993	Sequence 30993,
	6	73.2	56.3	874	20	US-10-363-345A-30994	Sequence 30994
	7	62	47.7	874	20	US-10-363-345A-30995	Sequence 30995,
ი	œ	62	47.7	874	20	US-10-363-345A-30996	Semience 30996

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22 2 2 4 4			25.7 25.4 25.4	28.3 28.3 27.8 27.7 27.7
1010 2107 560 2079 16018 16018	1489 1786 1806 3807 993	882 47988 385 1194 539 1866 17083	1,095 1595 1595 1077 771 878 878 852 1911	3288 3288 3630 632 486 9025608 2412 2959
		17 17 19 19 19	19 19 17 17 19 19	19 19 19 15 17 19
US-09-735-056-29 US-10-425-115-62599 US-10-424-599-55478 US-10-156-761-1755 US-09-764-869-1384 US-10-091-504-1384 US-10-227-577-1384	-10-425-115-171 -10-437-963-228 -10-739-930-505 -10-739-930-505 -10-739-930-505 -10-282-122A-26 -10-437-963-107	US-10-402-842-34 US-10-402-842-1 US-10-767-701-28894 US-10-156-761-3451 US-10-437-963-82849 US-10-437-963-84852 US-10-437-963-2791	-10-437-963 -10-437-963 -10-424-598 -10-260-238 -10-767-701 -10-437-963 -10-425-118	-10-7 -10-4 -10-4 -10-1 -10-1 -10-2
Sequence 29, Appl. Sequence 62599, A Sequence 52478, A Sequence 1755, Ap Sequence 1384, Ap Sequence 1384, Ap	171 228 505 505 107	1, 288 288 345 828 848 79		1, App 1, App 1, App 12593, 169387, 1614, A e 1, App e 1, App 1034, A 62213,

ALIGNMENTS

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GENERAL INCOMPATION:

APPLICANT: REED, JOHN C.

APPLICANT: REED, JOHN C.

APPLICANT: KE, NING

APPLICANT: GODZIK, ADAM

ITITLE OF INVENTION: APOPTOSIS MODULATOR BCL-B AND

ITITLE OF INVENTION: USING SAMB

PILE REFERENCE: 087102-0272558

CURRENT APPLICATION NUMBER: US/10/071,174

CURRENT FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: 60/267,166

PRIOR APPLICATION NUMBER: 20/267,166

PRIOR FILING DATE: 2001-02-07

NUMBER OF SEQ ID NOS: 36

SOFTMARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 887

TYPE: DNA

ORGANISM: Homo sapiens

US-10-071-174-1
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US-10-071-174-1
                                                                                Matches 127;
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                                                                                                       Query Match
Best Local Similarity
242 TCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC
                      1 TCCGCCTACCTCGGCTACCCCCGGGAACCGCTTCGAGCTGGTGGCGGCTGATGGCGGATTCC 60
                                                                                   Conservative
                                                                                                       88.3%;
96.9%;
                                                                                0,
                                                                                                     Score 114.8; DB 1
Pred. No. 1.9e-25;
                                                                                Mismatches
                                                                                                                           DB 16; Length 887;
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US-10-092-154-311
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SEQ ID NO 311
LENGTH: 548
                                                                                                                  GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 311
LENGTH: 548
TYPE: DNA
TYPE: DNA
                                                                                                                                                                                      Sequence 311, Appropriation No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
                                                                 CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
                                 Prior Application removed - See File Wrapper or Palm SOFTWARE: PatentIn Ver. 2.0
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LOCATION: (53)
OTHER INFORMATION: n
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OTHER INFORMATION: n
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
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NAME/KEY: SITE
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LOCATION: (26)
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                                                                                                                                                                                       Application US/10092154
o. US20030054375A1
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92.9%;
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Pred. No. 3.5e-21;
0; Mismatches 8
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RESULT 5
US-10-363-345A-30993/c
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; Publication No. US20040234960A1
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US-09-912-599-3
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SOFTWARE: Pate
SEQ ID NO 3
FNGTH: 522
                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PT044P1
CURRENT APPLICATION NUMBER: US/09/912,599
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: PCT/US01/03080
PRIOR PILING DATE: 2000-01-31
PRIOR PPLICATION NUMBER: 60/179,487
PRIOR PELING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/180,697
PRIOR APPLICATION NUMBER: 60/180,697
PRIOR FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Bcl-2-like Polynucleotides, Polypeptides, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09912599 Patent No. US20020106731A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                    LENGTH: 522
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                       GTTCGAGCTGGTGGCGCTGATGCCGGATTCCGTGCTCTCCGACAGCCCCGGCCCCACCT
                                                                                                         GGGGCAGAGTGGTGACGTCGTGACCTTCGCAGGGACGCTGCT 103
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96.1%;
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Pred. No. 3.5e-21;
0; Mismatches 8
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RESULT 6
US-10-363-345A-30994
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                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 30994
LENGTH: 874
ORGANISM: Artificial Sequence
PRAFFIED ONA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Pier
APPLICANT: Kurt Herlin
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                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Method for determining the degree of methylation of defined TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3 FILE REFERENCE: E01/1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Method for determining the degree of methylation of defined TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3 FILE REFERENCE: E01/127
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
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APPLICANT: Christian Pie
APPLICANT: Kurt Berlin
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ORGANISM: Artificial Sequence
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                                                                                                                                        TCCGCCTACCTCGGCTACCCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGGATTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGACGCTGCT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCTCTCCGACAGCCCCGGCCCCACCTGGGA-GNAGTGGTGACGCTCGTGACCTTCGCA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC 60
                                                                            GTGCTCTCCGACAGCCCCGGCCCCACCTGGGA-GNAGTGGTGACGCTCGTGACCTTCGCA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTACTCTCCGACAACCCCGACCCCACCTAAAACAAAATAATAACGCTCGTAACCTTCGCA
                                                                                                                    TCCGCCTACCTCGACTACCCCGAAAACCGCTTCGAACTAATAACGCTAATAACGAATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Christian Piepenbrock
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                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.3%;
77.1%;
                                                                                                                                                                                                                56.3%;
77.1%;
                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                Score 73.2; DB 20; Pred. No. 7.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 73.2; DB 20;
Pred. No. 7.7e-13;
0; Mismatches 29;
                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (Homo
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                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                  874;
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                                                                                                                                                          US-10-363-345A-30996
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US-10-363-345A-30996/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30996, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30995, Application US/10363345A Publication No. US20040234960A1 GENERAL INFORMATION:
                                                                              Best Lo
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LENGTH: 874
                                                                                                                                                                                                                                                              SEQ ID NO 30996
LENGTH: 874
TYPE: DNA
                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                     APPLICANT: Kurt Berlin TITLE OF INVENTION: Method for determining the degree of methylation of defined TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3 FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: E01/1227
FULL REFERENCE: E01/1227
CURRENT FAPPLICATION NUMBER: US/10/363,345A
CURRENT FALLING DATE: 2003-03-03
UNMBER OF SEQ ID NOS: 40712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) OTHER INFORMATION: CpG-island No: 30995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) OTHER INFORMATION: CpG-island No: 30996
                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                        FEATURE:
                                                                        Local Similarity
les 94; Conserv
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534 TICGITTATTICGGTTATTICGGGAATCGTTTCGAGTTGGTGGCGTTGATGGCGGATTTC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GTGCTCTCCGACAGCCCCGGCCCCACCT-GGGAGNAGTGGTGACGCTGGTGACCTTCGCA 119
                                      μ
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                                 TCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC 60
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                                                                              Conservative
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71.88;
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Pred. No. 1.9e-09;
                                                                              Score 62; DB 20;
Pred. No. 1.9e-09;
D; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-742-161-1
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US-10-742-161-1/c
; Sequence 1, Application US/1074
; Publication No. US20040120898A1
; GENERAL INFORMATION:
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                                          Matches
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Best Local (
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                                      Local Similarity 55.0 nes 71; Conservative
                                                                                                                                                                                                                                                                                                        LENGTH: 3288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
APPLICATION NUMBER: US/08/620,694
APPLICATION NUMBER: USSN 08/538,765
APPLICATION NUMBER: USSN 08/410,535
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spriggs, Melanie
Fanslow, William
TITLE OF INVENTION: Novel Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yao, Zhengbin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
1 TCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/742,161 FILING DATE: 18-Dec-2003 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Immunex Corporation STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/10742161
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                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                           STRAIN: HVS13 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (206
                                                         28.3%;
                                    Score 36.8; DB 19; Length 3288; Pred. No. 0.073; O; Mismatches 58; Indels 0;
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, NAME/KEY: CDS
; LOCATION: 121..2715
; SEQUENCE DESCRIPTION: SEQ
US-10-742-372-1
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US-10-742-372-1/c
  Query Match
Best Local Similarity
Matches 71; Conserv
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Publication No. US20040120899A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/742,372

FILING DATE: 18-Dec-2003

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE, DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fanslow, William
TITLE OF INVENTION: Novel Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2552 TCCTCCTCCGTGAGCCACTCGGGGGGGGCTGCGGGGAGCTCCTGGAGATGTAGCCCTGGTCC 2493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GGACGCTGC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCTCGGC 2424
                                                                                                                                                                                            ORGANISM: Mouse
STRAIN: HVS13 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3288 base pairs
                     28.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Melanie
Score 36.8; DB 19;
Pred. No. 0.073;
0; Mismatches 58;
                                                                                                           ID NO:
                                                                                                           ۳.
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                                           Length 3288;
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Conservative

Indels

0,

Gaps

0;

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US-10-425-115-169387

Sequence 169387, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                      RESULT 12
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US-10-437-963-12593/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bookharov, Andrey F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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                                                                                                                                                                                                                                                                                                                       123 ACGCTGC 129
                                                                                                                                                                                                                                                                                                                                                                                          63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 28.0%;
Similarity 55.1%;
                                                                                                                                                                                                                                                                                                                                                        GCCGACCGCCGCCGCCAGCGCCTCGGCGTCGGGAAACCCGCCTCCGCCGCCGCGGGG
                                                                                                                                                                                                                                                                                                                                                                                        GCTCTCCGACAGCCCCGGCCCCACCTGGGAGNAGTGGTGACGCTCGTGACCTTCGCAGGG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barbazuk, Brad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36.4; DB 19;
Pred. No. 0.095;
0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3630;
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                                                                                                                                                                                                                                                                                                                                                                                                                           913
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US-10-156-761-1614
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                                                                                                                                                                                                                                                                                                                                              APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1614
LENGTH: 486
TYPE: DNA
ORGANISM: Streptomyces avermitilis
                                                                                                                                Matches
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                                                                                                                                                               Query Match
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                               FEATURE:
NAME/KEY: CDS
LOCATION: (1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451
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405 CATCCTCGCCGACTCCTGGCGGCAGGCGGCTCCGCCCCGAC 445
                             72 CAGCCCCGGCCCCACCTGGGAGNAGTGGTGACGCTCGTGAC 112
                                                                                   12 CGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGGTGATGGCGGATTCCGTGCTCCCGA 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68; Conservative
                                                                                                                                60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 CCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGTGCTCTC
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                                                              CGGCTTCGCCTGGGTCCGGGTCCGGCTCGTGGCGCTGGAGGACGAGGCCGAACTGCGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGCGGCGGCGACGCCACCTCGCCCTCCTCGCGGCGTCCGCGGCCGCCGCCGCCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                Conservative
                                                                                                                                               27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.8%;
55.7%;
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                                                                                                                                               Score 36; DB 15; Pred. No. 0.15;
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Pred. No. 0.13;
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                                                                                                                                Mismatches
                                                                                                                                41;
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                                                                                                                                                               Length 486;
                                                                                                                                Indels
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                                                                                                                                Gaps
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RESULT 14 US-10-156-761-1/c

Sequence 1, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO

ISHIKAWA, JUN HORIKAWA, HIROSHI

SHIBA, TADAYOSHI

APPLICANT:

APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIKA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262

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LENGTH: 9025608
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: misc feature
LOCATION: (4187715)
OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
                                        ; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-10-260-238-1034
                                                                                                    PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 1034
LENGTH: 2412
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1034, Application US/10260238 Publication No. US20040016025A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                       APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
FILE REFERENCE: 60111-NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 CGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTCGATGGCGGGATTCCGTGCTCTCCGA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Budworth, Paul R.
Moughamer, Todd G.
Briggs, Steven P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cooper, Bret
Glazebrook, Jane
Goff, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                       Provart, Nicho
Ricke, Darrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Katagiri,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.7%; Score 36; DB 15; Length 90 ilarity 59.4%; Pred. No. 0.066; Conservative 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fumiyaki
  27.2%;
Score 35.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 15; Length 9025608;
DB 17;
Length 2412;
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                                                                                                                                                   Best Local Similarity 60.6%; Pred. No. 0.2; Matches 57; Conservative 0; Mismatches
 1590
                                                                          1530 CCCCGTCGGCGAGCACGCCAACATCTTCGGCGCGGGCCTGAAGATGGCGGACCGGGT 1589
                                     63 GCTCTCCGACAGCCCCGGCCCCACCTGGGAGNAG 96
                                                                                                                3 CGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCGT
GGTGACCGTGAGCCCCGGCTACCTCTGGGAGCTG 1623
                                                                                                                                                     37;
                                                                                                                                                     Indels
                                                                                                                                                     0
                                                                                                                                                 Gaps
                                                                                                                62
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Search completed: June 7, 2005, 18:04:27 Job time: 133.203 secs

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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         G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
      45.8
45.4
43.6
36.8
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27.2	27.2	27.5	27.7	27.7	27.8	27.8	27.8	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.3	28.3	28.3	28.3	28.3
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ALIGNMENTS

	FEATURES source	TITLE JOURNAL COMMENT	RESULT 1 AA09865 LOCUS LOCUS DEFINITION ACCESSION VERSION VERSION VERSION VERVWORDS SOURCE ORGANISM . REFERENCE AUTHORS
/organism="Homo sapiens" /mol_type="mRNA" /mb_xref="GDB:3804118" /db_xref="GDB:3804118" /db_xref="HQBB:3804118" /db_xref="HQB:3804118" /clone="nMAGB:489531" /sex="female" /dev_stage="adult" /lab_host="DH10B" /clone=lib="Soares_pregnant_uterus_NbHPU" /clone=lib="Soares_pregnant_uterus_NbHPU" /clone=lib="Soares_pregnant_uterus_NbHPU" /clone=lib="Soares_pregnant_uterus_NbHPU" /clone=lib="Soares_pregnant_uterus_NbHPU" /clone=lib="Goares_pregnant_uterus_NbHPU" /clone="Organ:uterus_NbHPU" /clone="Goares_pregnant_uterus_NbHPU" /clone="Goares_pregnant_	Tel: 314 286 1800 Fax: 314 286 1810 Email: estGwatson.wustl.edu Email: estGwatson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 81. Location/Qualifiers 1130	Hultman, M., Kucaba, T., Rifkin, L., Rohlfing, T. , Waterston, R., Willia erck EST Project (1995) (1995) Hson RK University School of Multiple Stark Parkway, Box 850:	AA098865 AA098865 ZK84f02.sl Soares pregnant_uterus_NDHPU Homo sapiens cDNA clone AA098865 AA098865 AA098865 AA098865 AA098865 CST. SST. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 130) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

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RESULT 2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 206)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                    est@watson.wustl.edu
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone lib="Soares fetal liver_spleen INPLS S1"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen INPLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5'
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/clone="IMAGE:428828"
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/db_xref="GDB:1328597"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylis Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y. Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Scl Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCi Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALDU4990 339 bp mRNA linear EST 21-APF vf22b11.x1 Knowles Solter mouse unfertilized egg Mus musculus clone IMAGE:836445 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 339)
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                                                                                                                                                                                                                                                                                                                                                                                            data is from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/WashU-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:496661
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization. Library
                                                                         eggs.
                                      5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTT-3'. cDNAs were cloned into the MluI/SalI sites of a modified pBluescribe
                                                                                         /note="Organ: unfertilized egg; Vector: pBluescribe (modified); Site_1: MluI; Site_2: SalI; Cloned unidirectionally from mRNA prepared from 5000 unfer
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                                                                                                                                                                                                                                                      'mol_type="mRNA"
'strain="C57BL/6J x DBA/2J
                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                        clone_lib="Knowles Solter mouse unfertilized egg"
                                                                                                                                                                            tissue_type="unfertilized'
lab_host="DH10B"
                                                                                                                                                                                                                   clone="IMAGE:836445"
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96.6%;
using commercial linkers 1.0 kb."
                                                                               Primer: SalI(dT):
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Rodentia;
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Pred. No. 5.4e-09;
D; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C.A., Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnaelgsun.grc.nia.nih.gov Plate: K0267 row: E column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Other_ESTs: K0267E03-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 448)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Dawood B. Dudekula Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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/note="Vector: psport1 (Invitrogen); Site_1: Sall; Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Unfertilized Egg"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                  (Long)
                                                                                                                                                                                                                                                                                                                                      /clone_lib="NIA Mouse Unfertilized Egg cDNA Library
(Lono)"
                                                                                                                                                                                                                                                                                                                                                                                                                  clone="NIA:K0267E03 IMAGE:30051122"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain="C57BL/6J"
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Pred. No. 0.0054;
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Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C.A., Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K0293B04-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus musculus cDNA clone NIA:K0293B04 IMAGE:30053583 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
Other_ESTs: K0293B04-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0293 row: B column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Systematic Analyses of NIA Mouse Unfertilized
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/note-"Vector: pSPORT1 (Invitrogen); Site_1: Sal1; Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics. National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                             /clone lib="NIA Mouse Unfertilized Egg cDNA Library (Long)"
                                                                                                                                                                                                                                             /db_xref="niaEST:K0293B04-5N"
/db_xref="taxon:10090"
/clone="NIA:K0293B04_IMAGE:30053583"
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                                                                                                                                                                                                  lab host="DH10B"
                                                                                                                                                                                                                    tissue_type="Unfertilized Egg"
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Pred. No. 0.0054;
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Query Match
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                                                                                                                                                                                                                                                        Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                           Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R. Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
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AI505208.1 GI:4403059
EST.
                                                                                          data is from the 3'
Seq primer: Primer I
                                                                                                                                  MGI:606172
This clone was previously sequenced on
                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vq73g11.x1 Knowles Solter mouse
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                          primer: Primer name ambiguous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus (house mouse)
                                         quality sequence stop:
Location/Qualifiers
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organism="Mus musculus"
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Pred. No.
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                                                                                                                                         only, this new
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RESULT 6 AI505208

FEATURES

COMMENT

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SOURCE KEYWORDS VERSION ACCESSION DEFINITION Pocus

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Other_ESTs: K0274C06-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
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98
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 524)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Stagg, C.A., Martin, P., Aiba, K., Tanaka, T. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA560564 524 bp mRNA linear K0274C06-5N NIA Mouse Unfertilized Egg cDNA Library musculus cDNA clone NIA:K0274C06 IMAGE:30051773 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA560564
                                                                                                                                                                                                                                           Seq primer: M13 Reverse
High quality sequence =
                                                                                                                                                                                                                                                                          National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, U Email: cdnaelgsun.grc.nia.nih.gov plate: K0274 row: C column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCGCCTACCTCGGCTACCCCGGGAACCCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGACGCT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGCTCTCCAAAGACCAAGACTTCAGCTGGAGCCAACTGGTGATGCTCCTGGCCTTCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTCCTTCTGCGAAAGCCGGGGCAATCGCCTGGAGCTGGTGAAACAGATGGCAGATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGACGCT 410
                                                                                                                                                                                                                                         quality sequence stop: 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="NIA:K0274C06 IMAGE:30051773"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
/clone_lib="NIA Mouse Unfertilized Egg cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
/clone_lib="Knowles Solter mouse_2 cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J x DBA/2J
/db_xref="taxon:10090"
                                                                                                          /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:K0274C06-5N"
                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="IMAGE:1108004"
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67.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
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Pred. No. 0.0054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Indels
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mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 19-NOV-2002
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GTGCTCTCCGACAGCCCCGGCCCCACCTGG-GAGNAGTGGTGACGCTCGTGACCTTCGCA 119
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588 bp mRNA linear K0229B10-5N NIA Mouse Unfertilized Egg cDNA Library musculus cDNA clone NIA:K0229B10 IMAGE:30047445 5', CA557550
                                                                                                                  National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnaelgsun.grc.nia.nih.gov Plate: K0229 row: B column: 10
                                                                                                                                                                                                                                    Other_ESTs: K0229B10-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                           Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C.A., Martin,P., Aiba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
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                                                                                    primer: M13 Reverse
                                                            quality sequence
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Pred. No.
                                                         stop: 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murinae; Mus.
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KEYWORDS SOURCE

ORGANISM

VERSION ACCESSION DEFINITION

REFERENCE

AUTHORS

TITLE

COMMENT

JOURNAL

FEATURES

source

organism="Mus musculus"/

RESULT 8

Ś 밁 ঠ 밁 ORIGIN

Matches

Local

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ACCESSION
VERSION
KEYWORDS
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                           JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                AUTHORS
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                                                                           Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi, Wood,W.H. III, Becker,K.G. and Ko,M.S.H. Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 650)
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H3058C03-5 NIA Mouse 15K cDNA Clone
H3058C03 5', mRNA sequence.
BG080867
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                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pSPORT1 (Invitrogen); Site_1: Sall; Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs.

Double-granded cDNAs were synthesized with an Oligo(dT)
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|strain="C57BL/6J"
|db_xref="taxon:10090"
|db_xref="taxon:10090"
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'lab_host="DH10B"
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2001 this sequence version replaced gi:12563419
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Pred. No. 0.0054;
0; Mismatches 4
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RESULT 10
CF915355
                                                             VERSION
KEYWORDS
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           ORGANISM
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ON B0978E08-5 NIA Mouse Unfertilized E musculus CDNA clone NIA:B0978E08 IM CF915355 GF915355.1 GI:38186557 EST.
Mus musculus (house mouse)
M Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
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This clone set has been freely distributed to the community.
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
plate: H3058 row: C column: 03
plate: H3058 row: C column: 03
seg primer: -21M13 Reverse
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Contact: George J. Kargul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGCTCTCCGACAGCCCCGGCCCCACCTGG-GAGNAGTGGTGACGCTCGTGACCTTCGCA 119
                                                                                                                                                                                                                                                                                                                                                                                                     GGGACGCT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGCTCCCAAAGACCAAGACTTCAGCTGGAGCCAACTGGTGATGCTCCTGGCCTTCGCG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTCCTTCTGCGAAAGCCGGGGCAATCGCCTGGAGCTGGTGAAACAGATGGCAGATAAG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC 60
                                                                                                                                                                                                                                                                                                                                                 GGGACGCT 301
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Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT) Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 173-1749; (3) Genome-wide manning of meal-ored transcripts from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation or the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; This
clone is among a rearrayed set of 15,247 clones from 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="H3058C03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .ab host="DH10B"
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Pred. No.
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ized Egg cDNA Library (Long
E08 IMAGE:30479767 5', mRNA
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MEDLINE
PUBMED
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                    120
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294
                                                                                                                      61
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Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 649)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0978 row: E column: 08
Seq_primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 11 (9), 1553-1558 (2001)
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                                                                                                               GTGCTCTCCGACAGCCCCGGCCCCACCTGG-GAGNAGTGGTGACGCTCGTGACCTTCGCA 119
                                    GGGACGCT 127
                                                                               TTGCTCTCCAAAGACCAAGACTTCAGCTGGAGCCAACTGGTGATGCTCCTGGCCTTCGCG 293
                                                                                                                                                                                                      TCCGCCTACCTCGGCTACCCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC
GGGACGCT 301
                                                                                                                                                               TCCTCCTTCTGCGAAAGCCGGGGCAATCGCCTGGAGCTGGTGAAACAGATGGCAGATAAG 233
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 649
                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sall; Site_2: NotL; Mouse cDNA project by the Laboratory of Genefics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="NIA:B0978E08 IMAGE:30479767"
/dev_stage="Unfertilized Egg"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mol_type="mRNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="niaEST:B0978E08-5"
                                                                                                                                                                                                                                                                39.2%;
67.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xref="taxon:10090"
                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                    Score 51; DB 7;
Pred. No. 0.0054;
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                 41;
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ACCESSION
VERSION
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ORGANISM
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RS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garibboddi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kasasawa, Y., Kedzieraki, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Malteis, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Malteis, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.C., Ringwald, M., Shandaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Yang, L., Wang, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Adachi,J., Aizawa,K., Akimura, A. Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Makamura,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Saroer Subsideria, Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construc nonredundant cDNA library. Genome Res. 11 (2), 281-289 ( cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                      sequencing
10 (11), 1
                                                                                                                                                                                                                                                                                                                                                          Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new
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                                                                                                                                                                                 genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome
10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                        Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          758 bp mRNA linear ES AGENCOURT 30246635 NIH MGC 256 Mus musculus cDNA clone IMAGE 30937853 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 758)
NIH-MGC http://mgc.nci.nih.gov/.
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EST.
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Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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http://image.llnl.gov
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                                                                                                                                              quality sequence stop: 623
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/clone="IMAGE:30937853"
/lab_host="DH10B TonA"
                                           /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                     /organism="Mus musculus"
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/dev_stage="1 cell embryo"
/clone_lib="RIKEN full-length enriched,
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|strain="C57BL/6J"
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Rodentia;
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Cancer Institute / NIH
Bldg. 31 Rm.10A07 Betheeda, MD 20892
Email: cgapbe-remail.nih.gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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incte="Organ: ocyte; Vector: pExpress-1; Site_1: EcoRV; Site_2: Not1; cDNA was primed using oilgo-df primer: 5'-pGACTAGTTCTAGATCGCCACCGCCCCCT(7)5-3' and cloned into the EcoRV/Not1 sites of pExpress-1. Size-selection >0.5 kb resulted in an average insert size of 1.2 kb. This is a primarylibrary (normalized primary library is NIH MGC 257) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library"
                                                                                                                                                                                                         /lab_host="DH10B TonA"
/clone_lib="NIH_MGC_256"
                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GTGCTCTCCGACAGCCCCGGCCCCACCTGG-GAGNAGTGGTGACGCTCGTGACCTTCGCA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 23
High quality sequence stop: 417.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution informatifound through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: NDAM1193 row: h column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 770)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGENCOURT 30256532 NIH MGC 256 Mus musculus cDNA clone IMAGE:309\overline{3}6954 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTCCTTCTGCGAAAGCCGGGCAATCGCCTGGAGCTGGTGAAACAGATGGCAGATAAG 131
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                                                                                                                                                                                                                               /mol_type="mRNA"
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Site_2: Not1; cDNA was primed using oligo-dT primer:
Site_2: Not1; cDNA was primed using oligo-dT primer:
Site_3: Not1; cDNA was primed using oligo-dT primer:
Site_5: pGACTAGTTCTAGATCGCCGAGCGGCCGCCCT[7]25-3; and cloned into
                                                                                                             the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 resulted in an average insert size of 1.2 kb. This is a primarylibrary (normalized primary library is NIH MGC 25 and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library"
                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
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Pred. No. 0.
                          Score 51;
Pred. No.
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tart: 23
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                                                Length 770
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1 TCCGCCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCC

Similarity

Conservative

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KEYWORDS
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AUTHORS
TITLE
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Best Local Similarity
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                                         61 GTGCTCTCCGACAGCCCCGGCCCCACCTGG-GAGNAGTGGTGACGCTCGTGACCTTCGCA 119
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                                                                                                                                                                                      86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
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High quality sequence stop: 666.
Location/Qualifiers
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CO814648.1 GI:51033274
EST.
Mus musculus (house mouse)
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Mational Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 772)
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                                                                                        TCCTCCTTCTGCGAAAGCCGGGGCAATCGCCTGGAGCTGGTGAAACAGATGGCAGATAAG
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                                                                                                                                                                                      Conservative
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the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb
resulted in an average insert size of 1.2 kb. This is a
primarylibrary (normalized primary library is NIH MGC 257)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"
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Qy 120 GGGACGCT 127
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Db 318 GGGACGCT 325
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